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GenCore version 5.1.6
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protein search, using sw model OM protein October 22, 2004, 23:04:28 ; Search time 33 Seconds (without alignments) 1309.131 Million cell updates/sec Run on:

US-10-681-223-2 2362 1 MAFARRLIRGPLSGPLLGRR......SREKVLQTVLSLIQNSFSEP 449 Title: Perfect score:

BLOSUM62 Scoring table: Sequence:

283416 segs, 96216763 residues Gapop 10.0 , Gapext 0.5 Searched: of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	707 30 30 15 14.	Query Match	Length	DB	r.	50 cm
S 1 11 11 11 11 11 11 11 11 11 11 11 11	301 301 155 44.5	Match		DB	1	コウランド・カナ・ シュ
10 m 4 m 9 c m 6 c l c m 7 m 7 m 7 m 7 m 7 m 7 m 7 m 7 m 7 m	301 155 54.5 143.5		- 1	i	U.L.	Description
0 m 4 l 9 c a a o d c m s	155 54.5 44.5 143	12.7	274	~	027	thymidylate kinase
K4U9CB60H7K	54.5 44.5 143		196	Ŋ	E69257	thymidylate kinase
4769897654	143	•	217	7	F82788	thymidylate kinase
N 9 C B B O H C B F	143	6.1	210	N	T41553	
9 C B B O H O M 7			189	(7	F90227	thymidylate kinase
7 B 6 0 H 7 E 7	131	5.5	237	0	10	dTMP kinase (EC 2.
B & O H A W 4			205	7	A75165	thymidylate kinase
80428			205	N	A71177	probable thymidyla
04787		5.3	212	7	A82128	
4005	123.5		210	7	S28955	dTMP kinase (EC 2.
200	\sim		234	7	D90518	
e -	120		212	7	866058	thymidylate kinase
,	19.5	5.1	204	Н	KIVZSW	
ť			188	73	F64336	kinase (EC
5		5.0	216	٦	KIBYT8	kinase
9	۲.		195	0	H70383	dylate
7			213	7	G64853	
8	7.	5.0	213	(1	D90813	thymidylate kinase
6	7		213	~	H85672	
20	117	5.0	211	N	F86674	thymidylate kinase
٦		4.9	218	~	T24244	hypothetical prote
7	115.5	4.9	205	C)	G72170	K2R protein - vari
3	115.5	4.9	205	7	A36854	thymidylate kinase
4	115.5	4.9	205	N	10	dTMP kinase (EC 2.
	115	4.9	738	~	AB2899	primosomal protein
	115	4.9	763	~	C97674	primosomal protein
27	113	4.8	513	~	S75604	pantothenate synth
æ	α.	4.8	1089	~	to	
29 1.	110.5	4.7	1504	7	12	FK506 polyketide s

thymidylate kinase	probable multi-dom	dIMP kinase (EC 2.	probable 268 ATP/u	DNA-directed DNA p	thymidylate kinase	glutamate dehydrog	thymidylate kinase	thymidylate kinase	dTMP kinase (EC 2.	dTMP kinase (EC 2.	UDP-N-acetylmuramo	signal recognition	signal recognition	ATP-dependent heli	hypothetical prote
B95108	T50568	C97976	T48743	A40597	B71814	S18609	B83655	G81700	A84971	AG3375	H95079	AI1299	AI1671	AF0526	A34728
	7	7	7	7	7	Н	7	N	C)	~	~	(1)	~	~	7
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212 2	1334	212	471	921	19	43	21	20	21	21	4	4	4	œ	7
				4.4 921											
4.5	4.5	4.5	4.5		4.4	4.4	4.4	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3

ALIGNMENTS

RESULT 1 102097 + thumidylate kinase-related protein TKRD1 (imported) - Leishmania maior (strain Friedlir	ciedlir
C.Species: Leibhmania major	
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004 C:bocesion: B81456: T02797	
RiMyler, P.J.; Audleman, L.; devos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;	s, C.;
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999	
A,Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c	otein-c
A;Reference number: A81455; MUID:99178987; PMID:10077609	
A;Accession: A81456	
A;Status: preliminary	
A; Molecule type: DNA	
A;Residues: 1-274 <pyl></pyl>	
A; Cross-references: UNIPROT: 060970; GB: AE001274; NID: 93264850; PIDN: AAC24621.1; PID: 929	ID:929'
A; Experimental source: strain MHOM/IL/81/Friedlin	
C;Genetics:	
A; Gene: TXRP1	
A;Map position: 1	
	_

7; 184 RLQVGCAQVVPVPE---PPLHPVVPDLPSSVVFPDREAARAVLEECTSFIPEARAVLDLV 240 241 DQCPKQIQKGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGQWRXIFDDEPT 300 SATAAR----KNPVIVVEGLDGTGKTLVTRTLAEKLSGVAISTPPPQFTEIRNTFRGQEE 115 59 -----CSNFVRQAEALSTSA Gaps Indels 34; 12.7%; Score 301; DB 2; Length 274; 32.0%; Pred. No. 2.7e-15; tive 39; Mismatches 108; Indels 19 RSRLDCLKVLHAVEQSSPPPPWWTPD-Conservative Query Match Best Local Similarity Matches 85; Conserva 09 d ð à

301 IIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGL-QHLPPAHHPV 359 q à

360 YOWPEDLIKEPDLILLITVSPEERLORLOGRGMEKTREEAELEANSVFROKVEMSYORMEN 419 qq ð

116 AVARAFYSAANYIAAEGILAASQSSVVVVDRWWCSTCAMALA---NGCLYDSLPPSGAAV 172

d

420 PGCHVVDASPSREKVLQTVLSLIQNS 445 Q δ

RESULT 2

thymidylate kinase (tmk) homolog - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 C;Accession: B69257 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

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Rishe, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Char Jong, I.; Jeffriss, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett. R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: P90227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 ---DEPTIIRRAFYSLGNYIVASEIAKESAKS-PVIVDRYWHSTATYAIATEVSGGLQHL 352
                                                                                                                                                                                                                                                                               358 PVYQWPEDLL------KPDLILLITVSPEERLQRLQGRGMEKTREEAELEANSVFRQK 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 PPAHHPVYQW----PEDLLKPDLILLTVSPEERLQRLQGRGMBKTREEAELBANSVFRQ 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thymidylate kinase (tmK-1) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: F90227
                                                                             EPTIIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHH
                                                                                                                                                                                                                                                                                                                 ::::::||||::|||||:|||||3 KQNRGRLIVEFDRTTAIGKKIDDYLKESV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 QLNDQ----VIHLLFSANRWETIQYIYEQINKGVTCILDRY----AFSGIAFSAAKGLD--
                                                                                                                                                                                                                  69 EVDVLLRDRRQHVEDLIVPMIGRGAV---VILDRYFPSMVAY----QGAAGL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 OKGKFOVVAIEGLDATGKTTVTOSVADSL----KAVLLKSPPSCIGOWRKIFD-
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                                        --KSPPSCIGOWRKIF---
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Best Local Similarity 26.1%; Pred. No. 0.0012;
Matches 58; Conservative 39; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                     410 VEMSYQRMENPGCHVVDASPSREKVLQTVLSLI 442
                                                                                                                                                                                                                                                                                                                                                                                                                                       254 VVAIEGLDATGKTTVTQSVADSLKAVLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: dTMP kinase
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c;Species: Xylella fastidiosa
C;Species: Aylella fastidiosa
C;Species: B-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: F82788
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A8515; MUD:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Reference number: R82788
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-217 cSIM>
A;Cross-references: GB:AE003904; GB:AE003849; NID:g9105433; PIDN:AAF83390.1; GSPDB:GNO01
A;Experimental source: strain 9a5c
A;Experimental source: strain 9a5c
B;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carraro, Briones, M.R.; Bueno, M.R.P.; Canargo, L.E.A.; Carraro, D.M.; Carraro, Briones: Merseriara, V.C.A.; Ferri, P. Reinach, J. Reinach, June 2000
A;Experimental source: strain 9a5c
B;Simpson, A.J.M.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Mancius, E.J.; Kuranee, E.E.; Katajama, J.D.; Junqueira, M.L.; Kemper, B.L.; Katajama, J.P.; Krieger, J.E.; Kuranee, E.E.; Laig, C.J.; Junqueira, M.C.; Remper, B.L.; Katajama, J.P.; Krieger, J.E.; Martinos, E.R.; Authores Martins, E.M.; Matsukuma, A.Y.; Menc, C.F.; M.; Miraces, M.V.; Matsukuma, A.Y.; Menc, C.F.; M.; Miraces, M.Y.; Matsukuma, A.Y.; Med Oliveria, M.C.; de Oliveria, M.C.; de Oliveria, D. F.C.; Munes, L.R.; de Rosa Jr., V.E.; de Silvei, M.; Vallada, H.; Vallada, H.; Vallada, A.; Vallada, A.; Vallada, A.; Vallada, H.; Vallada, H.;
Glodek, A.; Zhou, L.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F. Bature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A;Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:030175; GB:AE001102; GB:AE000782; NID:g2689425; PIDN:AAB9116
C;Superfamily: dTMP kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 VVAIEGLDATGKTIVTQSVADSL----KAVLLKSP-PSCIGQWRKIFDDEPTIIRRAFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LIAVEGIDGAĞKTTIAAYIAELLKEKGYKVKVLKEPGDSKFG--KKİKSSEERLSPEEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.6%; Score 155; DB 2; Length 196; Best Local Similarity 28.6%; Pred. No. 0.00018; Matches 61; Conservative 37; Mismatches 75; Indels
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ETTVVVDASKPLEEVKEEVRKVIESFLNLKKNS 195
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Best Local Similarity
Matches 59; Conserv
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A, Residues: 1-196 < KLE>
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11;

Gaps

49;

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Algorithm of the EMBL Data Library, July 1999
Albestription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struck Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struck Description: A75165
Algorithm of A75167

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C;Species: Pyrococcus horikoshii
R;Saccession: A71177
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
DNA, Res. 5, 5-76, 1988
A;Title: Complete Sequence and gene organization of the genome of a hyper-thermophilic
B;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: A71177
A;Accession: A71177
A;Accession: DNA, MID:98344137; PMID:9679194
A;Accession: DNA, MID:9679194
A;A
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Note: this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 RELVLKNSIIDGSRISYEAEALLFAADRAEHVKKVILPALEKGKVVICDRYLYSSLAYOW 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -RAFYSLGNYIVASEIAKESAK-----SPVIVDRYWHSTATYAI 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATEVSGGLQHLPPAHHPVYQWPEDL----LKPDLILLLTVSPEERLQRLQGRGMEKTREE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 KGKEQVVALEGLDATGKTTVTQSVAD----SLKAVLLKSP-PSCIGOW-RKIFDDEPTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thymidylate kinase related (tmk) PAB0319 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                             C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: A75165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 KGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPT----II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----QGWDVLLTKEPTDTEFGRLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LEWLMQINSFAPRPDLAILLDLPVKESIRRTKARG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AELEANSVFRQKVEMSYQRMEN -- PGCHVVDASPSREKVLQTVLSLIQN 444
5.3%; Score 125.5; DB 2; 23.3%; Pred. No. 0.032; tive 44; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.4%; Score 127.5; DB Best Local Similarity 22.7%; Pred. No. 0.023; Matches 52; Conservative 43; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGYF--VVLEGIDGSGKTTQAKLLAEWFEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: dTMP kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: tmk-like; PAB0319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-205 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; anonymous, Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 R-----
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A;Gene: PH1695
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NyAlternate names: thymidylate Kinase

C;Species: Haemophilus influenzae

C;Species: Haemophilus influenzae

C;Species: Haemophilus influenzae

C;Accession: A64153

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Relschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Cocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kalley, J.M.; Weidman, J.D.; Gocayne, J.D.; Scott, J. Soutt, J. Pritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: A64153

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-237 <TIGR>
A;Gene: tmk

C;Genetics:
A;Gene: tmk
C;Function:
A;Pathway: nucleotide biosynthesis
C;Superfamily: dTMP kinase
C;Keywords: ATP; nucleotide binding; nucleotide biosynthesis; P-loop; phosphotransferase
C;Keywords: ATP; nucleotide-binding motif A (P-loop)
                           A,Status: preliminary
A,Aolecule type: DNA
A,Molecule type: DNA
A,Residues: 1-189 <KUR>
A,Cross-references: UNIPROT:Q9UXG7; GB:AE006641; NID:g13813955; PIDN:AAK41077.1; GSPDB:G
C,Genetics: LnK-1
C,Superfamily: dTMP kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAEKLRHLIKHBTEEPVTDKAELLML--YAARIQLVENVIKPALMQGKRVVGDRHDMSSQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 AVLDLVDQCPKQIQKGKFQVVAIEGLDATGKTTVTQSVADSL-----KAVLLKSPPSC- 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----IGQWRKIFDDEPTIIRRAFYSLGNYIVASEIAKESAKSP-----VIVDRYWHSTA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 TYAIATEVSGGLQHLPPAHHPVYQWPEDLL---KPDLILLITVSPEERLQRLQGRGMEKT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLLKPDLILLITVSPRERLORLOGRGMEKTREEAELEANSVFROKVEMSYORM-ENPGCH 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 QVVAIEGLDATGKTTVTQSVADSLKA------VLLKSPPS--CIGQWRKIFDDEPTIIRR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 AFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLOHLPPAHHPVYQWPE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 LLFAADREIHVNWLSKIKDADLIILDRYYFSSIAYQGALGVDEQWIKMVNSYFP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVRXMPNKSABENMKGKF--IVIEGLEGAGKSSAHOSVVRVLHELGIODVVFTREPGGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KLIAIEGIDGSGKTTLANLLKEHLESKMKLNVIVTREPPSEDIIKLIEKIGWNDP-ILLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
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                                                                                                                                                                                                                                                                                                                                                                           Score 143; DB 2; Length 189;
Pred. No. 0.0014;
2; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98; Indels
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Best Local Similarity 25.4%; Pred. No. 0.015;
Matches 59; Conservative 37; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVDASPSREKVLQTVLSLIQNS 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVDASKDKNEVLEQAIKIIQKN 187
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 24.3%;
Matches 49; Conservative 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
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ģ 302

63;

Length Indels 49

151

Σ

301

Length 205;

OY 302 I-RRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQH 351	C; Keywords: ATP; nucleotide binding; nucleotide biosynthesis; P-loop; phosphotransferas F;14-21/Region: nucleotide-binding motif A (P-loop)
60 DGSKISYBAEALLFAADRAEHVKKIILPALSEGKVUICDRYFYSI.	cal Similarity 24.3%; Pred. No. 0.047;
	CONSEIVALIVE 35; MISMACCHES 5/; INGELS 75; GAPS GKFQVVAIEGLDATGKTTVTQSVADSLRAVLLKSPPSCIGGWRKIFDD 2
400 LEANSVFRQKVEMSYQRMENPQCHVVDASPSREKVLQTVLSLIQN	3 KQNRGRLIVIEGLDRSGKSTQCQLIVDKLILNMKRLKLFKFPDRTTAIGKKI-DDYLTES
	QY 298EPTIIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYA 340
RESULT 9 A82128 thymidylate kinase VC2016 [imported] - Vibrio cholerae (strain N16961 serogroup 01)	341 IATEVSGGLQHLPPAHHPVYQWPEDLLKPDLILLITVSPERLQRLQGRGMEKTRE
C;bpectes: vlbrio cnolerae C;bate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C:Accession: A87128	DD 103 IAFSAAKGIDWEWCKSPDRGLTRPDLVIFLNVDPKIAAIKGQYGEKYE 151
Rifeidelberg, 'N.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.J., R.R.; Mekhanos, J.J.; Venter, J.C.; Fraser, C.M.	152 KIEMQEKVLKNLQRLQKEFREEGLEFITLDASSYALEDVDSQIVDLVSN
Navite: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A:Reference number: A82035; MUID:20406833; PMID:10952301	
A;Accesion: A82128 A;Accesius: pradiminary A;Molevule tvne: nna	thymidylate kinase (dtmp kinase) [imported] - Mycoplasma pulmonis (strain UAB CTIP) C.Species: Mycoplasma pulmonis C.Date: 04.May.2001 Heavier payiein 24.May.2001 Heavi chance 09.Jn.1_2004
A/Residues: 1-212 <hei> A/Cross-references: UNIPROT:Q9KQ12; GB:AE004276; GB:AE003852; NID:g9656555; PIDN:AAF9516</hei>	C, Date: J. Tringy_co. 1 # requesize_levision 24 ray_co. 1 # re. 1 # r
A/EXPETIMENTAL BOURCE: SEROGROUD OL; STRAIN N16961; DIOTYPE B. TOR C;Genetics: A;Gene: VC2016	Nucleic Acids Res. 29, 2145-2153, 2001. A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul. A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Map position: 1 C;Superfamily: dTMP kinase	A; Accession: D90518 A; Status: preliminary
Query Match 5.3%; Score 124.5; DB 2; Length 212; Best Local Similarity 24.1%; Pred. No. 0.04; Matches 53; Conservative 36; Mismatches 88; Indels 43; Gaps 7;	A,MOLECULE LYPE: UNA A,Residues: 1-234 «KUR» A,Cross-references: UNIPROT:Q98RP7; GB:AL445566; PID:g14089465; PIDN:CAC13225.1; GSPDB: A,Experimental source: strain UAB CTIP
QY 255 VAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGQW 291	C'Genetics: A;Genetic MYPU 0520 A;Genetic code: SGC3 C;Superfamily: dTMP kinase
QY 292 RKIFD-DEPTIIRRAFYSLGNYIVASBIAKESAKSPVIVDRYMHSTATYAIATEVSGGLQ 350 :	Query Match 5.2%; Score 123; DB 2; Length 234; Best Local Similarity 25.5%; Pred. No. 0.559; Matches 56; Conservative 43; Mismatches 75; Indels 46; Gaps 14;
QY 351 HLPPAHHPVYQWPEDLLKPDLILLLTVSPEBRLQRLQGRGMEKTREBABLEANSVFRQKV 410	TGKTTVTQSVADSLKAV
Db 113 IAPSTWQSLKQTALGDFKPDLTLYLDIDPKLGLERARGRGELDRIEKWDISFFERA 168	Db 16 ITPEGIDASGKTSLLAKLKAHVVQKNLQGKCTFTWEPGGRKSPEIQTIRHLILNKE 71
QY 411 EMSYQRMENPGCHVVDASPSREKVLQTVLSLIQNSFSE 448 DD 169 RERYLELANSDDSVVMIDAAQSIEQVTADIRRALQDWLSQ 208	Qy 299 PTIIRRAF-YSLGNYIVASEIAKESAKSPVIVDRYWHSTATY-AIATEVSGGL 349 :
RESULT 10	QY 350 QHLPPAHHPVYQWPEDLILLILIYYSPEERLQRIGGRGMEKTREEABLEANSVFRQK 409 ::::: ::
<pre>QIMP Kinase (EC 2.7.4.9) - Ilssion yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004 C:Accession: S28655</pre>	QY 410 VEMSYQRMENPGCHVVDASPSREXVLQTVLSLIQN 444
מאדיה מלוויסר	100 VINGIDFLAGIFFERÇANIFVLUASANVEBEIFBSVLUALAND 21
a Colloca	RESOLD 12 866058 thymidylate kinase tmk - Bacillus subtilis
A;Molecule type: mRNA Asesidues: 1-210 <aba> A;Cross-references: UNIPROT:P36590; EMBL:X65868; NID:g4973; PIDN:CAA46698.1; PID:g4974 C;Superfamily: dTMP kinase</aba>	C;Species: Bacillus subtilis C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S66058; D69724 R;Ogasawara, N.; Nakai, S.; Yoshikawa, H.

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C;Superfamily: dTMP kinase
Kstywords: ATP; mucleotide binding; nucleotide biosynthesis; P-loop; phosphotransferas:
F;11-18/Region: nucleotide-binding motif A (P-loop)
F;11/Pinding site: ATP (Lys) #status predicted
A;Cross-references: UNIPROT:P13410; GB:M35027; NID:g335317; PIDN:AAA48180.1; PID:g335528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EWBL:X16259; NID:g62231; PIDN:CAA34345.1; PID:g62232
R;Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.
submitted to the EMBL Data Library, March 1997
A;Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) stra:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A42531. WIND: 9102102. A1201922
A;Contents: annotation; possible protein-coding frames
A;Note: neither amino acid nor nucleotide sequence is given
S;Smith, G.L.; de Carlos, A.; Chan, Y. S.
Nucleic A;Gis Res. 17, 7581-7590, 1989
A;Title: Vaccinia virus encodes a thymidylate kinase gene: sequence and transcriptional
A;Reference number: S06181; MUID: 90016845; PMID: 2552411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N'Alternate names: thymidylate kinase
C;Species: Methanococous jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: F64336
R;Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.
                                A, Experimental source: strain Copenhagen
R, Smith, G.L.; Chan, Y.S.; Howard, S.T.
J. Gen. Virol. 72, 1349-1376, 1991
A, Title: Nuclectide sequence of 42kbp of vaccinia virus strain WR from near the right
A, Reference number: JQ1767; MUID:91259063; PMID:2045793
A, Accession: JQ1786
                                                                                                                                                                                                                                                                                                                                                                                                                                       J.P.; Paoletti,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 YIV------ASEIAKESAKS-PVIVDRYWHSTATYAIATEVSGGLOHLPPAHHPV 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 YQWPEDLLKPDLILLLTVSPEERLQRLQGRGMEKTREEAELEANSVFRQKVEMSYQRMEN 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 VVAIEGLDATGKTTVTQSVADSLKAVLLK--SPPSCIGQWRKIFDDEPTIIRRAFYSLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LIVFEGLDKSGKTTQCMNIMESIPANTIKYLNFPQRSTVTGKMIDDYLT--RKKTYN--D
                                                                                                                                                                                                                                                                                                             A; Residues: 1-204 <SMI>
A; Residues: 1-204 <SMI>
A; Cross-references: DDBJ:D11079; NID:g222717; PIDN:BAA01822.1; PID:g222737
A; Experimental source: strain strain WR
R; Goebel, 8.7.; Johnson, GF.; Perkus, M.E.; Davis, S.W.; Winslow, J.P.; Perkus, Virology 179, 247-266, 1990
A; Title: The complete DNA sequence of vaccinia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Cross-references: EMBL:U94848; PIDN:AAB96539.1
A)Experimental source: strain Ankara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 28.09
Matches 51; Conservative
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A: Residues: 1-204 <SM2>
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                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: MVA161R
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        DNA Res. 1, 1-14, 1994

A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chrom A;Reference number: 865967; MUID:96051385; PMID:7584024

A;Reference number: 865967; MUID:96051385; PMID:7584024

A;Reference number: 865967; MUID:96051385; PMID:7584024

A;Reference number: 866058

A;Retaus: preliminary; nucleic acid sequence not shown; translation not shown

A;Residues: 1-212 < codAs

A;Rocoss.references: UNIPROY:P37537; EMBL:D26185; NID:9467326; PIDN:BAA05264.1; PID:94674

A;Rocoss.references: UNIPROY:P37537; EMBL:D26185; NID:9467326; PIDN:BAA05264.1; PID:94674

A;Rocos: reference: UNIPROY:P37537; EMBL:D26185; NID:9467326; PIDN:BAA05264.1; PID:94674

A;Rocos: reference: UNIPROY:P37537; EMBL:D26185; NID:9467326; PIDN:BAA05264.1; PID:94674

A;Rocos: reference: UNIPROY:P37537; EMBL:D26185; NID:946737

A;Rocos: Septimer: Solutilet, S; Bruschi, C,V; Caldwell, B.; Capuano, V.; Carter, N.M.; Characroic, C.; Furitato, M.; Furington, J.; Ferrari, E.

A;Authors: Rouleger, D; Fritz, C; Furitato, M.; Furitato, M.; Holsappel, S.; Hosono, S.; Hullo, M.; Rocetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lapidus, A.; Lapidus, A.; Lapidus, A.; Lapidus, A.; Lapidus, A.; Sakon, T.; Ayauthors: Labidus, A.; Codeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, A; Winters, P.; Voshikawa, H.F.; Zumstein, B.; Poshikawa, H.; Danchin, A.; Tosato, V.; Voshikawa, A; A; Aranaka, T.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Voshikawa, A; A; Accession: D69724

A; Accession: D69724

A; Accession: D69724

A; Reference number: A69580; MUID:98044033; PMID:9384377

A; Rocossion: D69724

A; Rocossion: 
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A,Cross-references: GB:Z99104; GB:AL009126; NID:G2632267; PIDN:CAB11804.1; PID:G2632295
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GTMP kinase (EC 2.7.4.9) - vaccinia virus

GTMP kinase (EC 2.7.4.9) - vaccinia virus

N.Alternate naems: A48R protein; SalFIIR protein; thymidylate kinase

N.Alternate naems: A48R protein; SalFIIR protein; thymidylate kinase

N.Alternate naems: A48R protein; SalFIIR protein; thymidylate kinase

A.Note: host Homo sapiens (man)

C.Saccesion: B42522; JQ1786; S60181; T37434

R.Gochel, S.J.; Johnson, G.P.; Perkus, M.E.; Davis, S.W.; Minslow, J.P.; Paoletti, Viroloy 179; 517-563, 1990

A.Title: Appendix to "The complete DNA sequence of vaccinia virus".

A.Reference number: A42501

A.Recession: E42522

A.Molecule type: DNA

A.Residues: 1-204 <GOE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: nucleotide binding; P-loop F;10-17/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 ---PGCHVVDASPSREKVLQTVLSLIQNSFSE 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: dTMP kinase
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á 311

61

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A; Molecule type: DNA
A; Residues: 1-216 <BREL:
A; Cross-references: EMBL: X01783
A; Note: the authors translated the codon TGG for residue 197 as Cys
R; Huang, M.E.; Manus, V.; Chuat, J.C.; Galibert, F.
Yasat 12, 869-875, 1996
A; Title: Analysis of a 62 kb DNA sequence of chromosome X reveals 36 open reading frame
A; Reference number: S71676; MUID: 96437976; PMID: 8840504
                                                                                                                                                                                                                                                                     A;Accession: S71679
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Job time : 36 secs
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                                                                                                 A;Title: Complete genome sequence of the methanogenic archaeon, methanocucus juminus as, Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: F64336
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: DNA
A;Residues: J-188 BBUL>
A;Molecule type: DNA
A;Residues: J-188 BBUL>
A;Genetics: A;Map position: FOR275602-276168
A;Coss-references: UNIPROT:657741; GB:U67484; GB:L77117; NID:g1591009; FIDN:AAB98278.1;
C;Genetics: A;Map position: FOR275602-276168
A;Start codon: TG
C;Superfamily: dTMP kinase
C;Keywords: nucleotide binding; P-loop; phosphotransferase
F;11-18/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dTMP kinase (EC 2.7.4.9) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein J1715; protein YJR057w; start control protein CDC8; thymidyla C;Species Saccharomyces cerevisiae
C;Decies Saccharomyces cerevisiae
C;Date: 28-Aug-1985 #sequence revision 19-Oct-1995 #text change 09-Jul-2004
C;Accession: S57076; A00683; Ā26127; S23299; S71679; S23301
K;Huang, M.E.; Chuat, J.C.; Gallbert, F.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S57055
A;Accession: S57076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Molecule type: DNA
A, Residues: 1-216 < MANA
A, Residues: 1-216 < MANA
A, Residues: 1-216 < MANA
A, Cross-references: UNIPROT: P00572; EMBL: Z49557; NID:g1015724; PIDN: CAA89585.1; PID:g101
B, Jong, A.Y.S.; Kuo, C.L.; Campbell, J.L.
J, Biol. Chem. 259, 11052-11059, 1984
A, Title: The CDG gene of yeast encodes thymidylate kinase.
A, Reference number: A00683; MUID:84289538; PMID:608527
A, Reference number: A00683; MUID:84289538; PMID:608527
A, Residues: 1-187, V. 189-216 < Johns
A, Residues: 1-187, V. 189-216 < Johns
A, Residues: BMBL: K02116; NID:g172985; PIDN:AAA35158.1; PID:g172986
A, Cross-references: EMBL: K02116; NID:g172985; PIDN:AAA35158.1; PID:g172986
A, Rochstein, R.; Helms, C.; Rosenberg, N.
A, Rochstein, R.; Helms, C.; Rosenberg, N.
A, Fittle: Concerted delations and inversions are caused by mitotic recombination between A, Reference number: A26127; MUID:87172788; PMID:3550432
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, G
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | ::: | | : | | | : | : | DRIEHTKLIKEELKKRDVVCDRYLYSSIAYQSVAGVDENP-----IKSINRYALKP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLILLLITUSPEERLQRLQGRGMEKTREEAELEANSVFRQKVEMSYQRM-ENPGCHVVDAS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYIVASEIAKESAKS-PVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVYQWPEDLLKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 188;
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Mol. Cell. Biol. 4, 583-590, 1984
A,Tille: Saccharomyces cerevisiae CDC8 gene and its product.
A,Reference number: S23299; MUID:84191140; PMID:6371491
A,Accession: S23299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 118.5; DB 2;
Pred. No. 0.096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 KKSVEEVHNEIIGYLKN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -PSREKVLQTVLSLIQN 444
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illarity 23.9%;
Conservative 4:
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A;Residues: 1-108;134-216 <ROT>
A;Cross-references: BMBL:M15468
R;Birkenmeyer, L.G.; Hill, J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Reywords: ATP; nucleotide binding; P-loop; phosphotransferase; pyrimidine deoxynucleo;12-19/Region: nucleotide-binding motif A (P-loop)
A.Residues: 1-216 - CHUA>
A.Residues: 1-216 - CHUA>
A.Cross-references: EMBL:L47993; NID:g1019675; PIDN:AAB39283.1; PID:g1019679
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C.Genetics:
C.Genetics: MIPS:YJR057w
A.Genetics: SGD:S0003818; MIPS:YJR057w
A.Cross-references: SGD:S0003818; MIPS:YJR057w
A.Map position: 10R
C.Superffamily: GTMP kinase
C.Scycriffamily: GTMP kinase
C.Scycriffamily: GTMP kinase
C.Scycriffamily: ATMP hucleotide binding: P-loop; phosphotransferase; pyrimidine deoxynucl
F:12-19/Region: nucleotide-binding motif A. (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --TVKFQEKVKQT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 IRRA---FYSLGNYIVASEIAKESAKSP-VIVDRYWHSTATYAIATEVSGGLQHLPPAHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVYQW---PE-DLLKPDLILLITVSPEERLQRLQGRGMEKTREEAELEANSVFRQKVEMS
                                                                                                                                                                                                                                                                                                                                                                                            Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SDQAIHLLFSANRWEIVDKIKKDLLEGKNIVMDRÝVYSGVAÝSAÁKGTNŐ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 MDLDWCLQPDVGLLKPDLTLFLSTQDVDNNAEKSGFGDERYE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 GKFQVVAIEGLDATGKTTVTQSVADSLK--AVLLKSPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 YQ-----RMENPGCHVVDASPSREKVLQTVLSLI
                                                                                                                                                                                                                                                                                                                                                                                                5.0%; Score 118.5; Di
25.0%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             37; Mismatches
                                                                                                                                                                                                                                                                                                                                  F;18/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             completed: October 22, 2004, 23:32:46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 22, 2004, 20:21:58 ; Search time 157 Seconds (without alignments) 1645.498 Million cell updates/sec Run on:

US-10-681-223-2 2362 1 MAFARRLERGPLSGPELGRR.....SREKVLQTVLSLIQNSFSEP 449 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ofpfd7 mus musculu	Aah57565 mus muscu	um au	Q6zru2 homo sapien	17 hom	e mus mus	_		7 xanth		030175 archaeoglob			Q61016 picrophilus		Oguxg7 sulfolobus	Q72n19 leptospira	9	Q9cke9 pasteurella	Q8leb4 arabidopsis			Q6nis4 corynebacte	Cae49210 corynebac	Q83hb8 tropheryma	Q83fm3 tropheryma				Ę	
SUMMARIES	ID	PFG	AAH57565	Q9DC34	Q6ZRU2	BAC87217	062316	060970	Q96ALB	KTHY XANAC	KTHY XANCP	KTHY_ARCFU	KTHY XYLFA	KTHY XYLFT		KTHY SCHPO	KTH1_SULSO	Q72NL9		KTHY PASMU	m	KTHY PYRFU	Q8SS <u>2</u> 2	Q6NIS4	CAE49210	KTHY TROWB		KTHY METMA	Q6F0 <u>E</u> 1	Q9AQD5	Q6MUI5	CAE76699
	DB	2	7	7	N	7	7	7	7	-1	Н	~	Н	Н	7	Н		7	~	Н	~	Н	7	~	~	н	н		N	~	~	7
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d	Query Match	71.3	71.3	65.7		62.1	•		12.3				•			•	•	•	•	•	5.9	-	-	2.6	-	-	-		-	-	-	
	Score	ന	68	1552	46	46	7.	301	σ	169.5	'n	5	•	m.	14	•	4	4	142	7	-	'n	13	m	31.	30.	•	30.	29.	$^{\circ}$		CI .
	Result No.		2	e	4	5	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31

0975e6 sulfolobus	Q9vle9 pyrococcus	Q6cc22 yarrowia li	Q8vi75 mus musculu	P44719 haemophilus	Q6fsb3 candida gla	059366 pyrococcus	Q9kgi2 vibrio chol	Q6cw62 kluyveromyc	Q80ht9 vaccinia vi	Q8fin9 escherichia	Q80ds7 cowpox viru	Q98rf7 mycoplasma	Q9p2h5 homo sapien
KTH1_SULTO	KTHY_PYRAB	Q6CC22	IPO4_MOUSE	KTHY HABIN	Q6FSB3	KTHY PYRHO	KTHY VIBCH	Q6CW62	Q80HT9	KTHY ECOL6	Q80D <u>S</u> 7	KTHY MYCPU	UB35_HUMAN
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190	202	204	1082	210	218	205	212	208	227	213	227	234	1017
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127.5 5.													

ALIGNMENTS

Q6PFG7 ID Q6	SPEG7	PRELIMINARY;	PRT;	417 AA.			
AC	SPFG7;		•				
ΓĮ	05-JUL-2004 (TrEMBLrel		Created)				
H			Last	Last sequence update)	_		
DŢ	05-JUL-2004 (TrEMBLrel.		Last	annotation update)	(e)		
DE	Tyki protein.						
ď	Name=Tyki;						
SO	Mus musculus (Mouse)						
Ö	Eukaryota; Metazoa;	.; Chordata;		Craniata; Vertebrata; Euteleostomi;	ta; Euteleos	stomi;	
ပ္ပ	Mammalia; Eutheria; Rodentia;	, Rodenti		gnathi; Muri	dae; Murinae	e; Mus.	
ŏ	NCBI TaxID=10090;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=C57BL/6; TISSUE=Mouse;	SSUE=Mons	e;				
RX	MEDLINE=22388257; PubMed=12477932;	PubMed=12	477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	eingold E	.A., Grou	se L.H., Der	ge J.G.,		
RA	Klausner R.D., Col	lins F.S.	, Wagner	L., Shenmen	C.M., Schule	er G.D.,	
RA:	Altschul S.F., Zee	berg B.,	Buetow K.	H., Schaefer	C.F., Bhat	N.K.,	
RA	Hopkins R.F., Jord	an H., Mo	ore T., M	ax S.I., Wan	g J., Hsieh	ч.,	
E.	Diatchenko L., Mar	usina K.,	Farmer A	.A., Rubin G	.M., Hong L		
RA	Stapleton M., Soar	es M.B.	Bonaldo M	.F., Casavan	T.L., Sche	setz T.E.,	
KA.	Brownstein M.J., U	sdin T.B.	, Toshiyu	ki S., Carni	ncı P., Pran	., c.,	
RA S	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,	ano N.A.,	Peters G	J., Abramso.	n R.D., Mul.	lany S.J.,	
ξ.	Bosak S.A., McEwan	. P.J., MC	Kernan K.	U., Malek U.,	A., Gunaratı	Je P.H.,	
KA G	Figurates S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	Y K.C., H	ale S., G	arcia A.M., (iay L.U., Hi	11YK S.W.,	
2 6	Fahour I Holton B	My D.M.	TELETIFICATION OF THE PROPERTY	ייה הים 'יינים	mine o nomi	,	
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2 Z	Blakeslev R.W. To	nchman T.	W. Green	E.D. Dicks	DOULERLY G.		
P.A	Rodriguez A C Gr	imwood T	Schmitz	T. Myers R	M. Butterf	ield Y S.	
R A	Krzywinski M.T. S	kalska II.	Suliems	D.E. Schnel	nch A. Sche	in J.E.	
RA	Jones S.J. Marra M.A.	Δ Σ					
Z	"Generation and in	itial ana	lvsis of	and initial analysis of more than 15,000 full-length human	.000 full-le	ength human	۲,
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E L	Proc. Natl. Acad. Sci. II.S. A.	S II S		99:16899-16903(2002)	. (2		
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RP	SECTIONS PROM N. A.						
R C	STRAIN=C57BL/6; TISSUE=Mouse;	SSUE=Mous	. 0				
R.A	Strausberg R.;						
RL	Submitted (SEP-2003) to the EMBL/GenBank/DDBJ	3) to the	EMBL/Gen	Bank/DDBJ dat	databases.		
DR	EMBL; BC057565; AAH57565.1;	H57565.1;	•				
DR	InterPro; IPR00006	2; Thymid	ylate_kin				
DR	Pfam; PF02223; Thymidylate_kin; 1.	midylate_	kin; 1.				
SO	SEQUENCE 417 AA;	46646 M	W; 978DE	DOAA83F12A	CRC64;		
ÓΜ̈́	Query Match Best Local Similarity		Score 1 Pred. N	71.3%; Score 1684; DB 2; 77.1%; Pred, No. 3.5e-115;	Length 417;		
Σ̈́	Matches 323; Conser	vat	38; Mism	atches 54;	Indels	4; Gaps	
ò	27 MAPPCRFVL	ELPDCTLAH	FALGADAPG	MAPPCRFVLELPDCTLAHFALGADAPGDADAPDPRLAALLGPPERSYSLCVPVTPDAGCG	LGPPERSYSLCV	/PVTPDAGCG	98
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REPARAINE-C57BL/6. TISSUE-Mouse;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. Buetwe K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B. Buetwe K.H., Schaefer C.F., Bhat N.K.,

RA Altschark L., Maruaina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Weiner S.G., Abramson R.D., Mullahy S.J.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Wordiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA "Generation and initial analysis of more than 15,000 full-length human
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ARVRAARLHQRILHQLRRGPPQRCQLLRLLCYCPGGQAGGAQQGFLLRDPLDDPDTRQAL
                                                      LELLGACQEAPRPHLGEFEADPRGQLWQRLWEVQDGRRLQVGCAQVVPVPEPPLHPVVPD
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Sciurognathi; Muridae; Murinae; Mus
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%; Pred. No. 3.5e-115;
38; Mismatches 54; Indels
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46646 MW; 978DE9D0AA83F12A CRC64;
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Last annotation update)
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID≃10090;
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STRAIN=C57BL/6; TISSUE=Mouse;
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77.1%;
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SEQUENCE 417 AA; 46646 M
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Best Local Similarity 77.15
Matches 323; Conservative
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Submitted (SEP-2003)
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Mus musculus (Mouse)
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01-0707-2001 (TrEMBLrel. 17, Last sequence update)
01-0707-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200004E04 product:thymidylate kinase family LPS-inducible
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                                        ARVRAARLHQRLLHQLRRGPFQRCQLLRLLCYCPGGQAGGAQQGFLLRDPLDDPDTRQAL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Solurognathi, Muridae, Murinae, Mus
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Nature 420:563-573(2002).
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STRAIN=CSTBL/64; TISSUE=Lung;
STRAIN=20499374; PubMed=11042159;
Carriino: P., Shibata Y., Hayatsu N., Sugahara Y., Sh
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=CSPEL/60, TISSUE=Lung;
MEDILINE=21085660; Pubmed=11217851;
RIKEN FANTOM CONSORTIUM;
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STRAIN-CS7BL/6J; TISSUE=Lung;
MEDLINE=99279253; PubMed=10349636;
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Fori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Muramatsu M., Hayashizaki Y.,
Summirted GUUL-2000 to the EMBL/GenBank/DDBJ databases.

R HSSP, P00572: 1TMK.

R HSSP, P00572: 1TMK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QKGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPTIIRRAFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLGNYIVASBIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVYQWPEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLGNYLVASEIAKESTNFPVIVDRYWHSTATYAIATEVSGGLQYLPPAHHPVYQWPGDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPDLILLLTVSPEERLQRLQGRGMEKTREEAELEANSVFRQKVEMSYQRMENPGCHVVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                       MEDLINE=20530913; PubMed=11076861; Sasaki N., Carninci P., Shibata K., Ttoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata Y., Ttoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Wirk integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new gegenome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.7%; Score 1552; DB 2; Length 395; 77.8%; Pred. No. 1.6e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62F338B649983DF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P00572; ITMK.

MGD; MGI:99830; Tyki.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0004798; F:thymidylate kinase activity; IEA.

GO; GO:0006233; P:dTP biosynthesis; IEA.

GO; GO:0006235; P:GTP biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.8%; Pred. No. 1.6e ive 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000062; Thymidylate kin.
223: Thymidylate kin; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02223; Thymidylate_kin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 AA; 44085 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 77.8%
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89
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61 RLAALLGPPERSYSLCVPVTPDAGCGARVRAARLHQRLLHQLRRGPFQRCQLLRLLCYCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GGQAGGAQQGFLLRDPLDDPDTRQALLELLGACQEAPRPHLGEFEADPRGQLWQRLWEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGAGGAQQGFLLRDPLDDPDTRQALLELLGACQEAPRPHLGEFEADPRGQLWQRLWEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGRRLQVGCAQVVPVPEPPLHPVVPDLPSSVVFPDREAARAVLBECTSFIPEARAVLDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGRRLQVGCAQVVPVPEPPLHPVVPDLPSSVVFPDREAARAVLEECTSFIPEARAVLDLV
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02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ4609 fis, clone TESTI2021654, weakly similar to Mus musculus
thymidylate kinase family LPS-inducible member (Tyki).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAFARRILRGPLSGPLLGRRGVCAGAWAPPCRFVLELPDCTLAHFALGADAPGDADAPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Testis;

Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S., Tanehori K., Ishibashi T., Sato H., Hotuta T., Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Kawatsuma M., Takahashi-Fujii A., Oshima A., Eugiyama A., Kawakami Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (UUL-2003) to the EMBL/GenBank/DDBJ databases.

BMBL; AK127983; BAC87217.1;

Kinase.
                                                                                                                                                                                                                                                                                                                bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 AA; 32645 MW; 4C7D0715B7B970C6 CRC64;
                                                                                                                                                                                                                                                                           Last annotation update)
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                                                                                                                                                                                                                                                   (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 DOCPKOIOKGKFOVVAIEGLDATGKTTVTOSVADSLKAV
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Pred. No. 2.3e-99;
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                                                                                                                                                                         303
                                                                                                                                                                                                                           (TrEMBLrel. 27, Created)
                                                                                                                                                                         PRT;
                                            393
                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, La
05-JUL-2004 (TrEMBLrel. 27, La
Hypothetical protein FLJ46098.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.1%;
99.6%;
                                            SPSRETVLOKVLELIOSS
SPSREKVLQTVLSLIQNS
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                                                                                                                                                                           PRELIMINARY;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 [1] SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Simi
Matches 278;
                                                                                                                                                                                                                              05-JUL-2004
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A Myler P.J., Audleman L., devos. T., Hixson G., Kiser P., Lemley C., Myler P.J., Audleman L., devos. T., devo
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                                                                                                                                                                                                                         REEAELEANSVFRQKVEMSYQRMENP----GCHVVD-----ASPSREKVLQTVLS 440
                                                                                                                                                                                                                                                                      241 DOCPKOIOKGKFOVVAIEGLDATGKTTVTOSVADSLKAVLLKSPPSCIGOWRKIFDDEPT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SATAAR----KNPVIVVEGLDGTGKTLVTRTLAEKLSGVAISTPPPQFTEIRNTFRGQEE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YQWPEDLLKPDLILLTVSPBERLQRLQGRGMEKTREEAELEANSVFRQKVEMSYQRMEN 419
   217 PPCI---KPVEBDLLMMNLLSFEEPFIL-----WANYLVASEIAKESTNFPVIVDRYWH 267
                                                                          STATYALATEVSGGLOHLPPAHHPVYQWPEDLLKPDLILLTVSPEERLORLOGRGMEKT 394
                                                                                                                    -----CSNFVRQAEALSTSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 IIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGL-QHLPPAHHPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 YRWPEDLPAPDAGFLLCVDEAVRVARIRRRAPEDA-EERRLSSQREMRCVAMEAYRR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420 PGCHVVDASPSREKVLQTVLSLIQNS 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Friedlin;
MEDLINE=99178987; PubMed=10077609;
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07,
25,
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Matches 85; Conservative
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                                                                                  335
                                                                                                                                                     268
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TISSUE=Testis;
Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
Tanai H., Watanabe S., Ishida S., Ono Y., Horura T., Watanabe M.,
Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Yamamoto J., Isono Y., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wamura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
"NEDO human CDNA sequencing project.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AKL27983; BAC87217.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAFARRILRGPLSGPLLGRRGVCAGAMAPPRRFVLELPDCTLAHFALGADAPGDADAPDP
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1466; DB 2; Length 3 Pred. No. 2.3e-99; o; Mismatches 1; Indels
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Liee (Gi., O'Brien W.E.;
Submitted (GAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; L32973; AAA58770.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                              32645 MW; 4C7D0715B7B970C6 CRC64;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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GO; GO:0016301; F:kinase activity; IEA.
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01-NOV-1996 (TrEMBLrel. 01, Lr
01-JUN-2003 (TrEMBLrel. 24, Lr
Thymidylate kinase homologue.
Name-Tyki;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.1%;
Best Local Similarity 99.6%;
Matches 278; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142; Conservative
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Best Local Similarity
Matches 142; Conserv
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SEQUENCE FROM N.A.

SEQUENCE TO 33913 / NCPPB 528;

MEDLINB=22022145; PubMed=1202417; DOI=10.1038/417459a;

A da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A da Silva A.C.R., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A laves L.M.C., do Amaral A.M., Bertollini M.C., Camargo L.B.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciaphna L.P.,

Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Formighieri B.F., Franco M.C., Ferreira R.C.C., Ferro M.I.T.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.N.,

Martins E.C., Machado M.J., Madeira A.M.B.N., Martinez-Rossi N.N.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sana J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

A Trindade dos Santos M., Truffil D., Tsai S.M., White F.F.,

Schubal J.C., Kitalima V.P.,

Schubal J.C., Kitalima V.B.,

Schubal J.C.,

Schubal J.C.,

Schubal J.C.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 PVYQWPEDLL-----KPDLILLLTVSPEERLQRLGGRGMEKTREEAELEANSVFRQKV 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LIAIBGIDGAGKITILARRIAATLDAAGARVVLSKEPIN--GPWGTQLRQSAATGRLSAEE
                                                                                                                                                                                                                  HAMAP; MF 00165; -; 1.
InterPro; IPR00062; Thymidylate kin.
InterPro; Thymidylate kin.
InterPro; Thromidylate kin.
IGRFAMS; TIGR00041; DTMP kinase; 1.
PROSITE; PS01331; THYMIDYLATE KINASE; FALSE NEG.
ATP-binding; Complete proteome; Kinase; Nucleotide biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                    23 ATP (Potential).
24030 MW; 7C78722F1BCFA211 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.2%; Score 169.5; DB 1
Best Local Similarity 27.4%; Pred. No. 0.00023;
Matches 58; Conservative 37; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           442
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28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2004 (Rel. 45, Last annotation update)
Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 RTIFAALELPGKHVVDASADADSVLRQAHAII 196
                                modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@isb-sib.ch).
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      non-profit institutions as long
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227 AA;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SETAIN=306 / ATCC 13902 / XV 101;

MEDINRE-20202145; PubMed=12024217; DOI=10.1038/4174599;

A da Silva A.C.R., Ferro J.A., Refrach F.C., Farah C.S., Furlan L.R.,

A da Silva A.C.R., Almeida N.F.,

A da Silva A.C.R., Can Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F.C., Ciapina L.P.,

Carcelli R.M.B., Coulinho L.L., Cursino-Santos J.R., El-Dorry H.,

Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Formighieri E.F., Franco M.C., Graegio C.C., Gruber A.,

Formighieri E.C., Machadon M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machadus J.W., Menck C.F.M., Maryaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira W.R.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.;

Comparison, of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 EKTREEAELEANSVFROKVEMSYQRMENPGCHVVDASPSREKVLQTVLSLIQNSFSEP 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria; Gammaproteobacteria, Xanthomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.3%; Score 291; DB 2; Length 58; 100.0%; Pred. No. 4.8e-14; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C12029FED37F4BAC CRC64;
                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Thymidylate kinase (EC 2.7.4.9) (dTWP kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 AA
                                                58 AA
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                                                                                                                                                                                               Hypothetical protein (Fragment). Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kanthomonadaceae; Xanthomonas.
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Submitted (NOV-2001) to the
EMBL; BC016969; AAH16969.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 AA; 6653 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 417:459-463(2002).
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                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Prostate;
                                                                                                                                    01-DEC-2001
01-OCT-2002
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                Q96AL8
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(Rel. 40, Created)
                                                                                                                                                                                                               EMBL; AE001102; AAB91163.1; ~.
                                                                                                                                                                                                                                                                                                                                                                                                                                                61; Conservative
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                                        Nature 390:364-370(1997)
                                                                                                                                                                                                                            PIR; E69257; E69257.
HSSP; P37345; 5TMP.
TIGR; AF0061; -.
                                                                                                                                                                                                                                                                                                                                                                                        196 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                             Transferase.
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                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357
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 form dTDP in both de novo and
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MEDLINE-98049343; PubMed-9389475; DOI=10.1038/37052;
Klein H.-P., Clayfon R.A., Tomb J.-F., White O., Neterson J.D.,
Ketchum K.A., Dodson R.J., Gwinn M.L., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.R.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
Zhou L., Overbeck R., Gocayne J.D., Weidman J.F., McDonald L.A.,
Utteraback T.R., Cotton M.D., Spriggs T., Artiach P., Kaine B.P.,
Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,
Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                 HSSP; P37345; STMP.

HAMAP; MF 00165; -; 1.

HAMAP; MF 00165; -; 1.

PITCEPTEO, IPRO0062; Thymidylate kin.

Pfam; PF02223; Thymidylate kin; 1.

TIGREAMS; TIGR00041; DTMP kinase; 1.

PROSITE; PS01331; THYMIDYLATE KINASE; FALSE NEG.

ATP-binding; Complete proteome; Kinase; Nucleotide biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                                                                                                             7.0%; Score 166.5; DB 1; Length 227; 26.8%; Pred. No. 0.00038;
            salvage pathways of dTTP synthesis (By similarity). CATALYTIC ACTIVITY: ATP + dTWP = ADP + dTDP. SIMILARITY: Belongs to the thymidylate kinase family.
                                                                                                                                                                                                                                                                                                                                                                                          70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   254 VVAIEGLDATGKTTVTQSVADSL----KAVLLKSPPSCIGQW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (dTMP kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Buryarchāeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                   16 23 ATP (Potential).
227 AA; 24000 MW; BDB0D3C89E66753C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 VEMSYQRMENPGCHVVDASPSREKVLQTVLSLI 442
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CRAIFAALQLPGKHVIDASADADSVLRQAHAVV 196
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15-JUL-1999 (Rel. 38, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Probable thymidylate kinase (EC 2.7.4.9) (dTM)
Name=tmk; OrderedLocusNames=AF0061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 AA.
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 FUNCTION: Phosphorylation of dTMP to
                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                          35;
                                                                                                                                                                                       EMBL; AE012513; AAM43153.1; -.
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                           Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                      Transferase.
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030175;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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KTHY ARCFU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 OWPEDLL-KPDLILLITVSPEERLORLOGRGMEKTREEAELEANSVFROKVEMSYQRMEN 419
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MEDLINE=20366717; PubMed=10910347; DOI=10.1038/35018003;
MEDLINE=20366717; PubMed=10910347; DOI=10.1038/35018003;
Alvarenga R.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Bartos M.H., Bonacorsi E.D., Bordin S., Bove J.M., Briones M.R.S. Canargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
Woese C.R., Venter J.C.;
"The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
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Xanthomonadaceae; Xylella.
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                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: ATP + dTMP = ADP + dTDP.
-!- SIMILARITY: Belongs to the thymidylate kinase family.
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22349 MW; F9CF20D740A5A367 CRC64;
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InterPro; IPR000062; Thymidylate kin.
Pfam; PP02223; Thymidylate kin; 1.
TIGREAMS; TIGR00041; DTMP kinase; 1.
PROSITE; PS01331; THYMIDYLATE KINASE; 1.
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Xylella fastidiosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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RA Fraga J.S., Franca A.J.S., Ferreira V.C.A., Ferro J.A., RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., RA Garnier M., Goldman M.H.S., Gomes S.L., Gruber A., RA HO P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., RA Krieger J.E., Kuramae E.E., Lopes S.A., Lopes C.R., Machado J.P., RA Machado M.M., Madeira A.M.B.N., Madeira H.M.F., Marino C.L., Mardins E.A.L., Martins E.M.F., Martsukuma A.Y., Martins E.M.F., Martino C.L., Manch M. N., Martins E.M.F., Monceiro J.L.C., R.A., Mono D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Nhani A. Jr., Nobrega F.G., Muncs L.R., Oliveira M.A., Paris A., Paris A., Paris A., Paris A., Paris A., Peris G. G., G., Pereira H.A. Jr., Pesquero J.B., R.A. Quaggio R.B., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., A. Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Souza A.C.R., da Silva A.M., da Silva M.A., Varjoveira M.J., Silwa W.A. Jr., R.A. da Silva M.A., Varjoveira W.J., Ga Silva M.A., Varjoveira W.J., Catonia W.J., Ga Souza A.B., R.A. Varjada H.Y., Van Sluys M.A., Varjoveira J.S., Catonia W.J., Catone A.L., R.A. Zago M.A., Zatz M., Meddanis J., Setubal J.C., Nature 406:151-159(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: Phosphorylation of dTMP to form dTDP in both de novo and salvage pathways of dTTP synthesis (By similarity).
-!- CATALYTIC ACTIVITY: ATP + dTMP = ADP + dTDP.
-!- SIMILARITY: Belongs to the thymidylate kinase family.
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TIGREPAS, TIGRO041; DTMP Kinaes; 1.
PROSITE; PS01311; THYMIDYLATE KINAES; FALSE NEG.
ATP-binding; Complete proteome; Kinase; Nucleotide biosynthesis;
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5563ADA4F9D541AE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch)
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InterPro; IPR00062; Thymidylate kin.
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22436 MW;
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les 59; Conserv
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208 AA

STANDARD;

_KTHY_XYLFT Q87B89;

RESULT 13
KTHY XYLFT

10-OCT-2003 (Rel. 42, Created)

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Wan Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Moon D.H.,
Naita M.A., Lemos B.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,
Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.B.,
Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
da Cunha A.F., Fenille R.C., Ferro J.A., Fornighieri E.F., Kishi L.T.,
de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Xylella
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PROSITE; PS01331; THYMIDYLATE KINASE; FALSE NEG.
ATP-binding; Complete proteome; Kinase; Nucleotide biosynthesis;
                                                                                                                               Xylella fastidiosa (strain Temeculai / ATCC 700964).
Bacteria: Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 VVAIEGLDATGKTTVTQSVADSLKAVLL----KSPPSCIGQWRKIF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         salvage pathways of dTTP synthesis (By similarity).
-!- CATALYTIC ACTIVITY: ATP + dTMP = ADP + dTDP.
-!- SIMILARITY: Belongs to the thymidylate kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 ATP (Potential).
22455 MW; 254E0C9268E33633 CRC64;
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27.2%; Pred. No. 0.0072;
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10-OCT-2003 (Rel. 42, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
11hymidylate kinase (BC 2.7.4.9) (dTMP kinase)
Name=tmk; OrderedLocusNames=PD1569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 VEMSYQRMENPGCHVVDASPSREKVLQTVLSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP; MF 00165; -; 1.
InterPro; IPR000062; Thymidylate kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE012559; AA029411.1; -.
                                                                                                                                                                               Bacteria, Proteobacteria,
Xanthomonadaceae, Xylella.
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nes 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P37345; STMP
                                                                                                                                                                                                                                                    NCBI_TaxID=183190;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kitajima J.P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 IVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVYQWPED----LLK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 MHQKEI-KNHLINGVISDRYVFSSIAYQ-----GSGMEKRFKNMDETISWMLDVSRFIIM 122
                                                                                                                                                                                                                                                                                                                                                                                                                                      89
                                                                                                                                                                                     Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C., Schepers B., Dock C., Antranikian G., Liebl W.; "Genome sequence of Picrophilus torridus and its implications for life
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93003330; PubMed=1327149; Abaigar L.T., Yeh Y.I., Jong A.Y.; "Functional and structural conservation of Schizosaccharomyces pombe dIMP kinase gene."; Ediochim. Biophys. Acta 1132:222-224(1992).
                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                     Length 202;
                                                                                                          Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Picrophilaceae; Picrophilus.
                                                                                                                                                                                                                                                                                                                                                                                          71; Indels
                                                                                                                                                                                                                                                                                                PEAN, PF02223; Thymidylate kin, I.
TIGRFAMS; TIGR00041; DTMP kinase; 1.
PROSITE; PS01331; THYMIDYLATE KINASE; 1.
Complete proteome; Kinase; Transferase.
SEQUENCE 202 AA; 23548 MW; ECD5A5FC43B67EE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=tmp1, Synonyms=tmp; ORFNames=SPCC70.07c;
Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetes;
                                                                                                                                                                                                                               EMBL, AE017261, AAT43686.1; -. 101:9091-9096(2004).
EMBL, AE017261, AAT43686.1; -.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0004798; F:kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR
                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                  6.1%; Score 145; DB 2;
0.0%; Pred. No. 0.012;
ve 22; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-UN-1994 (Rel. 29, Created) 16-0C7-2001 (Rel. 40, Last sequence update) 16-0C7-2004 (Rel. 45, Last annotation update) Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDLILLLTVSPEERLQRLQGRGMEKTREEA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 POLITYLKIDPGIALKRINLKKNEKKNTDA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 AA
                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence
05-JUL-2004 (TrEMBLrel. 27, Last amotatic
Putative thymidylate kinase (BC 2.7, 4.9).
                                                                                                                                                                STRAIN=DSM 9790 / ATCC 700027;
PubMed=15184674;
                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.1%;
Best Local Similarity 30.0%;
                                                                                      OrderedLocusNames=PTO1101;
                                                                                                                                                                                                                                                                                                                                                                                           45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                     PRELIMINARY;
                                                                                                 Picrophilus torridus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
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SEQUENCE FROM N.A.
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                 NCBI_TaxID=82076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4896;
                                                                                                                                                                                                                        around pH 0."
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                                Q6L016;
                     261016
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WEDLINE=21948401; PubMed=11859360; DOI=10.1038/nature724;
WEDLINE=21948401; PubMed=11859360; DOI=10.1038/nature724;
WEDLINE=21948401; PubMed=11859360; DOI=10.1038/nature724;
WOOd V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Cdell C.,
Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbinowitsch E.,
Skelton J., Simmonds M., Squares R., Saeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
A raylor K., Taylor K., Tavey A., Walsh S.Y., Warren T., Whitehead S.,
Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Boffeu A., Cadleu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
A Lucas M., Rochet M., Gaillardin C., Moore K., Hurst S.M.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Dominguez A., Revuelta J.L., Moreno S., Ammistrong J., Forsburg S.L.,
A Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Borthi L., Lowe T., Moreno S., Ammistrong J., Forsburg S.L.,
Mathyle G., Mathyle R., Mathyle R., Mathyle R.,
Mathyle G., Nathyle Barrell B.G., Nurse P.,
Mathyle G., Mathyle R., Mathyle R.,
Mathyle M., Mathyle R., Mathyle R.,
Mathyle M., Mathyle M.,
Mathyle M.,
Mathyle M.,
Math This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibc.ch). 11; 297 ---DEPTIIRRAFYSLGNYIVASEIAKESAKS-PVIVDRYWHSTATYAIATEVSGGLQHL 352 62 3 KONRGRLIVIEGLDRSGKSTQCQLLVDKLISQHEKAELFKFPDRTTAIGKKIDDYLKESV 248 QKGKFQVVAIEGLDATGKTTVTQSVADSL----KAVLLKSPPSCIGQWRKIFD----TIQYIYEQINKGVT -> PSIYYRANQQRCN (in Ref. Gaps PIR; SL.

R HSSP; P00572; TTMK.

R GeneDB SPowbe; SPCC70.07c; -.

R GeneDB SPOwbe; SPCC70.07c; -.

R InterPro; IPR00062; Thymidylate kin.

DR InterPro; IPR00062; Thymidylate kin.

DR TIGREAMs; TIGR0041; DTMP kinase; 1.

DR PROSITE; PS01331; THYMIDYLATE KINASE; 1.

KM ATP-binding; Kinase; Nucleotide biosynthesis; Transferase.

NO BIND 14 21 SQHEKAE -> INMKRLK (in Ref. 1).

R PSI PSO STATE READ SQHEKAE -> INMKRLK (in Ref. 1).

R PSI STATE READ SQHEKAE -> INMKRLK (in Ref. 1).

R -> T (in Ref. 1). 49; DB 1; Length 210; -i- FUNCTION: Catalyzes the conversion of dTMP to dTDP.
-i- CAPALYTIC ACTIVITY: ATP + dTMP = ADP + dTDP.
-i- PATHMAY: Blosynthesis of dTMP from dTMP.
-i- SIMILARITY: Belongs to the thymidylate kinase family. Indels P -> T (in Ref. 1).
F -> L (in Ref. 1).
S -> YA (in Ref. 1).
H -> D (in Ref. 1).
N; 4266144AEDAB68CO CRC64; 6.1%; Score 144.5; DB 1; 26.1%; Pred. No. 0.014; iive 39; Mismatches 76; .. 24249 MW; EMBL, X65868; CAA46698.1; -. EMBL, AL023794; CAA19357.1; -. EMBL; S28955; S28955. PIR; T41553; T41553. Nature 415:871-880(2002). Conservative 210 AA; Similarity

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October 22, 2004, 23:32:53 ; Search time 104 Seconds (without alignments) 1397.766 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                              US-10-681-223-2
2362
1 MAFARRLIRGPLSGPLIGRR......SREKVLQTVLSLIQNSFSEP 449
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_Pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_PUB_COMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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					SUMMARIES		
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Result	ק קר	Query	Query Match Length DB	ä	Ę	Dogorintion	
	1000	110000	17817	1		rescribing	
Н	2362	100.0		14	US-10-277-032-2	Sequence 2, Appli	
2	2362	100.0		15	US-10-681-223-2	Sequence 2, Appli	
m	795.5	33.7	508	14	US-10-277-032-4	Sequence 4, Appli	
4	795.5	33.7		15	US-10-681-223-4	Sequence 4, Appli	
S	155	9.9		14	US-10-369-493-911	Seguence 911, App	
9	140	5.9		15	US-10-282-122A-67367	Sequence 67367, A	
7	131.5	5.6	205	15	US-10-282-122A-53917	Sequence 53917, A	
80	128.5	5.4		14	US-10-369-493-11256	Sequence 11256, A	
σ	128.5	5.4		16	US-10-437-963-196428	Sequence 196428,	
10	127.5	5.4		14	US-10-369-493-21577	Sequence 21577, A	
11	127	5.4		14	US-10-369-493-22800	Sequence 22800, A	
12	126.5	5.4		15	US-10-425-114-64336	Sequence 64336, A	
13	126	5.3		6	US-09-815-242-11027	Sequence 11027, A	

equence 58176 equence 1320, equence 20385 equence 61591 equence 77370		Sequence 2218 Sequence 3, A Sequence 1640 Sequence 1809 Sequence 70,	Sequence 10129, A Sequence 797, App Sequence 56520, A Sequence 2, Appli Sequence 194022, Sequence 18331, A Sequence 59458, A	equence 43 equence 113 equence 123 equence 41 equence 43 equence 43 equence 59 equence 10
-10-282-122A-5817 -10-369-493-1320 -10-369-493-20385 -10-282-122A-6159	-10-437-9 -10-156-7 -10-282-7 -10-369-4	S-10-369-493-221 S-10-754-929-3 S-10-437-963-164 S-10-369-493-180 S-10-369-493-70	9-815-242-101 10-369-493-79 10-282-122A-5 10-754-929-2 10-437-963-19 10-369-493-18	10.369.493.5938 10.369.493.6559 10.369.493.1259 10.493.123.11246 10.369.493.286 10.369.493.4190 110.369.493.4190 110.282.122A.4919 110.282.122A.4919
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APPLICANT: Ming-Hui WEI
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THERENOF
FILE REFERENCE: CLOO1305 DIV
CURRENT APPLICATION NUMBER: 2010/27,032
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: 09/984,880
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Score 2362; DB 14; Length 449;
Best Local Similarity 100.0%; Pred. No. 4.4e-201;
Matches 449; Conservative 0; Mismatches 0; Indels 0;
                     Sequence 2, Application US/10277032; Publication No. US20030087294A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: HomoSapien
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JS-10-277-032-2
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                                                                                          OWPEDILKPDLILLITVSPEERLORLOGRGMEKTREEAELEANSVFROKVEMSYORMENP 420
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Sequence 4, Application US/10681223
Publication No. US20040081999A1
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14;
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Pred. No. 9.8e-62;
0; Mismatches 4;
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                                                                                                                                                GCHVVDASPSREKVLQTVLSLIQNSFSEP 449
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48.1%;
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US-10-277-032-4
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US-10-277-032-4
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Subjection No. US20040081993A1

Subjection No. US20040081999A1

GENERAL INFORMATION:

APPLICATION

TITLE OF INVENTION:

TITLE OF INV
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            GGQAGGAQQGFLLRDPLDDPDTRQALLELLGACQEAPRPHLGEFEADPRGQLWQRLWEVQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GCHVVDASPSREKVLQTVLSLIQNSFSEP 449
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US-10-681-223-2
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254 VVAIEGLDATGKTTVTQSVADSL----KAVLLKSP-PSCIGQWRKIFDDEPTIIRRAFY 307
                                                                                                                                                                                                                                                  308 SLGNYIVASEI-AKES-----AKSPVIVDRYWHSTATYALATEVSGGLQHLPPAHHPVY 360
                                                                                                                                                                                                                                                                                                                                                        361 QWPEDLL-KPDLILLLTVSPEERLQRLQGRGMEKTREEAELEANSVFRQKVEMSYQRMEN 419
                                                                                                                                                                                                                                                                                                                                                                                         2 LIAVEGIDGAGKTTIAAYIAELLKEKGYKVKVLKEPGDSKFG--KKIKSSEERLSPEEEL
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                                                                                        40;
                                   Length 196;
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                                                                                                                                                                                                                                                                                   60 EL--FLKDREIDARENILPALQSGYAVVMDRYYFSNIAYQSARGIDARL-
                                                                                        Indels
                                 Query Match
6.6%; Score 155; DB 14;
Best Local Similarity 28.6%; Pred. No. 2.2e-05;
Matches 61; Conservative 37; Mismatches 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              420 PGCHVVDASPSRE----KVLQTVLSLIQNS 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 67367, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PLING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PRILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Yamamoto, Robert
Forsyth, R.
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SEQ ID NO 67367
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APPLICANT:
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APPLICANT:
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghon, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERBENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 911
LENGTH: 196
        ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 PKEVQKGKFQVIAIEGLDATGKTTLTQHFKSLSRLSSYSRHPSCIGGWRKIFDDEPTIIR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 RAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYPCIKFNYVASEIAKESPVIVDRYW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CTSFIPEARAVLDLVDQCPKQKGKFQVAIEGLDATGKTTTQQCTSFIPEARAVLDLVDQC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 795.5; DB 1
Pred. No. 9.8e-62;
0; Mismatches 4
TITLE OF INVENTION: ACID MOLECULES ENCODING
TITLE OF INVENTION: THEREDS
FILE REFERENCE: CLOO1305 DIV-II
CURRENT APPLICATION NUMBER: US/10/681,223
PRIOR APPLICATION NUMBER: 10/277,032
PRIOR PILING DATE: 2002-10-22
PRIOR PILING DATE: 2001-10-31
PRIOR PILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 911, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 RAFYSLGNYIVASEIAKESAKS-
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48.1%;
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Matches 177; Conserv
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US-10-369-493-911
                                                                                                                                                                                                                                                                                              SEQ ID NO 4
LENGTH: 508
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58; Conservative
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Best Local S
Matches 58
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### APPLICANT:
### CURRENT APPLICATION NUMBER:
### CURRENT PAPPLICATION NUMBER:
### CURRENT PAPPLICATION NUMBER:
### CURRENT PAPPLICATION NUMBER:
### CURRENT PAPPLICATION NUMBER:
### CONDO-03-21
### PRIOR PELING DATE:
### PAPPLICATION NUMBER:
### PAPPLICATION PAPPLICATION NUMBER:
### PAPPLICATION PAPPLICATION DATE:
### PAPPLICATION PAPPLICATION DATE:
### PAPPLICATION PAPPLICATION DATE:
### PAPPLICATIO
                          10;
                                                                                                                                                                                                                                              PVTDKAELIMLYAARIQLVENVIKPALAQGKWVIGDRHDMSSQAY-----QGGGRQLD- 148
                                                                                                                                                                                              PTIIRR---APYSLGNYIVASEIAKESAKSP-VIVDRYWHSTATYAIATEVSGGLQHLPP 354
                                                                                                                                                                                                                                                                                                             355 AHHPVYQWPEDLL---KPDLILLITVSPERLQRLQRCGMEKTREEAELEANSVFRQKVE 411
                                                                                                                                                                                                                                                                                                                                                      250 GKFQVVAIEGLDATGKTTVTQSVADSLKA-----VLLKSPPSC----IGQWRKIFDDE
                                                                                                                                   38 GKF--IVLEGIEGAGKTTARDSIVRALHAHGIHDIVFTREPGGTPLAEKLROLIKHETEE
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                          34; Gaps
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                          Indels
                          89;
                                                                                                                                                                                                                                                                                                                                                                                                                                 412 MSYQRM--ENPGCHVVDASPSREKVLQTVLSLIQ 443
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2; Mismatches 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 53917, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                             32;
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  27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Trawick, John
Carr, Grant
Yamamoto, Robert
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Best Local Similarity 22.4
Matches 51; Conservative
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Zyskind, Judith
                                   Conservative
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  Best Local Similarity
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                                   59.
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
ENGTH: 1999
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                                                                                                                                       TDSAYAMATLFALDRYDAKAVLGRYVGTSKV------VLLDRYVASNAAYSAAR---- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -LGNYIVASEIAKESAKSPVIVDRYWHSTATYALATEVSG 347
                                              --RYEQSIHAKLAQRALYGSMGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 IRRAFYSLGN-----YIVASBIAKESAK-----SPVIVDRYWHSTATYAIATEVSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 KGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 14; Length 199;
                                                                                                                                                                                                                                                                                                 394 TREEAELEANSVFRQKVEMSYQRMENPGCHV-VDASPS--REKVLQTV 438
                                                                                                                                                                                                                                                                                                                                      403 NSVFRQKVEMSYQRM--ENPGCHVV-DASPSREKVLQTVLSLI 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.4%; Score 128.5; DB 14;
26.0%; Pred. No. 0.0052;
ive 39; Mismatches 71;
                               2 IIAIEGIDGAGKNTLVSAIKERFDADVIGFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 196428, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihna
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11256, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Serven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: ELEANESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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                                                                                                                               -LKPDLILLLTVSPEERLORLOGRGMEKTREE 397
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                                                                             50 RELVLKNSIIDGSRISYEAEALLFAADRAEHVKKVILPALEKGKVVICDRYLYSSLAYQW 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 -PEDLLKPDLILLLTVSPEERLQRLQGRGMEKTREEAELEANSVFRQKVEMSYQRME--- 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::::::|||||:||:||:||:||3 KQNRGRLIVIEGLDRSGKSTQCQLLVDKLISQHEKAELFKFPGKSYFCFLADXLVTFTRX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 --PSCIGQWRKIFD------DEPTIIRRAFYSLGNYIVASEIAKESAKS-PVIVDRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 DRTTAIG--KKIDDYLKESVQLNDQ---VIHLLFSANRWETIQYIYEQINKGVTCILDRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94; Gaps
                                                                                                                                                        398 AELEANSVFRQKVEMSYQRMEN--PGCHVVDASPSREKVLQTVLSLIQN 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)...(259)
OTHER INFORMATION: unsure at all Xaa locations
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                                  --RAFYSLGNYIVASEIAKESAK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 22800, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
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Sequence 64336, Application US/10425114

Publication No. US20040034888A1

GRNERAL INFORMATION:

APPLICANT: Liu, Jingdong
                                                                                                                            342 ATEVSGGLQHLPPAHHPVYQWPEDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Schizosaccharomyces pombe
FEATURE:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 22.33
Matches 60, Conservative
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SEQ ID NO 22800
LENGTH: 259
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                                                                                                                                                                           110 ARGLS --
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                                303 R--
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APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Pinc
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERRINCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Serven C.
APPLICANT: Slater, Serven C.
APPLICANT: Slater, Serven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 IPEARAVLDLVDQCPKQIQKGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 EGWR--FPDRGT-----SVGQ-MISAYLANESELDDRTIHLLFSANRWEKRALMERKL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 SPEERLORLOGRGMEKTREEAELEANSVFROKVEMSYORMENPGCHVVDASPSREKVLOT 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 OPEKAAER-GGYGGER-YEKIE-----FOKKVGEHYHSLRDSTWKVVDGSLPMEVVEEQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 KGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPT----II 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 -AKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVYQW---PED-LLKPDLILLLTV
                                                                                                                                                                                                                                                                                                                                                                                                              Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.4%; Score 127.5; DB 14; Length 205; illarity 22.7%; Pred. No. 0.0067; Conservative 43; Mismatches 71; Indels 63;
                                                                                                                                                                                                                                                                                                                                                                                                            5.4%; Score 128.5; DB 16; Length
24.7%; Pred. No. 0.0073;
ive 39; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_92280C.1.pep
US-10-437-963-196428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 Q-WRKIFDDEPTIIRRAFYSLGNYIVASEIAKES
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Publication No. US20030233675A1
GENERAL INFORMATION:
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SEQ ID NO 21577
                                                                                                                                                                                                                                                                                                                                                                                                                                                           62; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 52; Conserv
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US-10-369-493-21577
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Carr, Grant
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APPLICANT:
APPLICANT:
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Best Local
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uB-10-

".EulCANT: Zhou, Yihua

APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Graen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 GRGALVVLEGLDRSGKTSQCARLLSFLKGKGYNAE----GWR--FPDRAT-----SV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 FSAAKGLD-----IEWCKAPENGLIAPDLVIYLDVQPEKAABR-GGYGGER-YEKI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AKSPVIVDRYWHSTATYAIA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 TEVSGGLQHLPPAHHPVYQW---PED-LLKPDLILLLTVSPEERLQRLQGRGMEKTREEA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 15; DB 15; Length 263; 11 12 25.5%; Pred. No. 0.012; Conservative 34; Mismatches 70; Indels 71;
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROKARYOCES

TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL
CURRENT PRINCADES: 2001-03-21
CURRENT PRINCADATE: 2001-03-21
PRIOR PPLICATION NUMBER: 60/2019, 078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/283,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-16
NUMBER OF SEQ ID NOS: 14110
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US-10-425-114-64336
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Carr, Grant J.
Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 GNYIVASELAKES----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays
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APPLICANT: Xu, H.

TITLE OP INVENTION: Identification of Essential Genes in Microorganisms
FILE REPREBACE: ELITRA.034-02-20
CURRENT APPLICATION NUMBER: 05/191,076
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-03-21
PRIOR PLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/230,335
PRIOR PLICATION NUMBER: 60/230,347
PRIOR PLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PLICATION NUMBER: 60/253,625
PRIOR PLICATION NUMBER: 60/253,625
PRIOR PLICATION NUMBER: 60/253,625
PRIOR PLICATION NUMBER: 60/257,931
PRIOR PLILING DATE: 2000-110-23
PRIOR PLILING DATE: 2000-12-22
PRIOR PLILING DATE: 2000-12-22
PRIOR PLILING DATE: 2000-12-20
PRIOR PLILING DATE: 2001-12-0-09
PRIOR PLILING DATE: 2001-12-0-09
PRIOR PLILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                            249 KGKFQVVAIEGLDATGKTTVTQSVADSL-----KAVLLKSPPSC-----IGQWRKIFDD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 LPPAHHPVYQWPEDLL---KPDLILLLTVSPEERLQRLQGRGMEKTREEAELEANSVFRQ 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 EPTIIRRAFYSLGNYIVASEIAKESAKSP-----VIVDRYWHSTATYAIATEVSGGLQH 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KGKR--IVİBGLEGAĞKSSAHQSVVRVLHELGIQDVVFTREPGGTPLAEKLRHLIKHETE
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                                                                                                                                                                                                                                      5.3%; Score 126; DB 9; Length 210; 26.1%; Pred. No. 0.0094; iive 32; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 KVEMSYQRM--ENPGCHVVDASPSREKVLOTVLSLIQN 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11027
LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 58176, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                         Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Liangsu
APPLICANT: Alamdio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Green C.
APPLICANT: Green C.
APPLICANT: Green C.
APPLICANT: Barry S.
APPLICANT: Green C.
APPLICANT: Barry S.
APPLICANT: Barry S.
APPLICATION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(5.205.)B
CURRENT APPLICATION NUMBER: US /10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1320
                                                                                                                                                                                                                                                                                                                                                             60 EPVTDKAELLML--YAARIQLVENVIKPALMQGKWVVGDRHDMSSQAY-----QGGGRQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 KGKFQVVAIEGLDATGKTTVTQSVADSL-----KAVLLKSPPSC----IGQWRKIFDD 297
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                                                                                                                                                                          91; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 5.3%; Score 125.5; DB 14; Length 205; l Similarity 23.3%; Pred. No. 0.01; 53; Conservative 44; Mismatches 71; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 DGSKISYEAEALLFAADRAEHVKKIILPALSEGKVVICDRYFYSSL-----
                                                                                                                      5.3%; Score 126; DB 15; Length 210; 26.1%; Pred. No. 0.0094;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Sequence 1320, Application US/10369493
, Publication No. US20030233675A1
; GENERAL INFORMATION:
                  ; TYPE: PRT; ORGANISM: Haemophilus influenzae
US-10-282-122A-58176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Pyrococcus horikoshii
US-10-369-493-1320
                                                                                                                      Query Match
Best Local Similarity
Matches 57; Conserva
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Best Local Similarity
Matches 53; Conserva
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US-10-369-493-1320
LENGTH: 210
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Search completed: October 22, 2004, 23:40:34 Job time : 107 secs

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Sequence 2, Appli
Sequence 4, Appli
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Sequence 28002, A
Sequence 2560, A
Sequence 2560, Ap
Sequence 2750, Ap
Sequence 2750, Ap
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Sequence 2751, Ap
Sequence 2711, Ap
Sequence 1721, Ap
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17231, A
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21572, A
25356, A
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25366, A
8, Appli
6, Appli
                                                                                                                          October 22, 2004, 23:05:48; Search time 29 Seconds (without alignments) 1026.786 Million cell updates/sec
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2362
1 MAFARRLIRGPLSGPLLGRR.....SREKVLQTVLSLIQNSFSEP
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5.1.6
Compugen Ltd.
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US-10-277-032-2
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US-09-252-991A-28002
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US-09-252-991A-25690
US-09-252-991A-25642
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US-09-252-991A-25765
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US-00-00-079-8
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Copyright (c) 1993 - 2004
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Length 449; Indels 0

Query Match 100.0%; Score 2362; DB 4; Best Local Similarity 100.0%; Pred. No. 2.2e-232; Matches 449; Conservative 0; Mismatches 0;

TYPE: PRT ORGANISM: HomoSapien US-09-984-880-2 09

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120

121 GGQAGGAQQGFLLRDPLDDPDTRQALLELLGACQEAPRPHLGFFEADPRGQLWQRLWEVO 180

GGQAGGAQQGFLLRDPLDDPDTRQALLELLGACQEAPRPHLGEFEADPRGQLWQRLWEVQ

121

DGRRLQVGCAQVVPVPEPPLHPVVPDLPSSVVFPDREAARAVLEECTSFIPEARAVLDLV

DGRRLQVGCAQVVPVPEPPLHPVVPDLPSSVVFPDREAARAVLEECTSFIPEARAVLDLV

181 181 241 241 420

QWPEDLLKPDLILLITVSPEERLQRLQGRGMEKTREEAELEANSVFRQKVEMSYQRMENP

IIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVY

301

300

DQCPKQIQKGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGOWRKIFDDEPT

NUCLEIC KINASE PROTEINS, AND USES	KINASE PROTEINS, S ENCODING HUMAN	880-2 O. Application US/09984880 O. 6489153 INFORMATION: NT: Ming-Hui WEI F INVENTION: ISOLATED HUMAN F INVENTION: THEREOF FINVENTION: THEREOF FERENCE: CLO01305	1017 1 109-984-880-2 109-984-880-880-2 109-984-880-880-8 1	RESULT 1 US-09-984-880-2 Sequence 2. Applicat Patent No. 6489153 GENERAL INFORMATION: APPLICANT: Ming-Hui TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: CLO	RESULT 1 US-09-984-1 Sequence Petent N GENERAL APPLICAL TITLE OI TITLE OI TITLE OI TITLE OI FILE REI
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Sequence 4, Application US/10277032

Sequence 4, Application US/10277032

Sequence 4, Application US/10277032

Patent No. 6664097

GENERAL INFORMATION:

APPLICANT: Ming-Hui WEI

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLO01305 DIV

CURRENT FILING DATE: 2002-10-22

PRIOR FILING DATE: 2001-10-21

PRIOR PLICATION NUMBER: 09/994,880

PRIOR FILING DATE: 2001-10-22

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PASLSEQ for Windows Version 4.0
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ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF
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Pred. No. 2.7e-72;
0; Mismatches 4;
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Pred. No. 2.7e-72;
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48.1%;
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    TITLE OF INVENTION: ACID MOLE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1305
CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 2001-10-
NUMBER OF SEQ ID NOS: 4
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Best Local Similarity 48.1
Matches 177; Conservative
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Best Local Similarity 48.1
Matches 177; Conservative
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ORGANISM: HomoSapien
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APPLICANT: Ming-Hui WEI
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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100.0%; Pred. No. 2.2e-232;
iive 0; Mismatches 0;
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TYPE: PRT
ORGANISM: HomoSapien
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QY 222 VLEECTSFIPEARAVLDLVDQCPKQIQKGKFQVVAIEGLDATGKTTVT 269	270 QSVADSLKAVLLKSPPSCIGGWRKIFDDEPTI-IRRAFYSLGNYIVASEIAKES ::	323 AKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVYQWPEDLLKP	Db 653 RRGAASEAPVLLIGETGTGKELLAHAIHSASPRAHKAFVSVNAAAIPESLLEA 705 Qy 370 DLILLLIVSPERRLQR	706 ELFGTAPGAFTG	Qy 402 ANSVFRQKVEM 412 	RESULT 6 US-09-632-553-3 ; Sequence 3, Application US/09632553 ; Patent No. 6689595 ; Remembat. INFORMATION.	APPLICANT: Pharmacia & Upjohn TITLE OF INVENTION: Crystallization and Structure Determination of TITLE OF INVENTION: Staphylococcus Aureus Thymidylate Kinase TITLE OF LASSENCE: 6245.NCP CURRENT APPLICATION NUMBER: US/09/632,553 CURRENT FILING DATE: 2000-08-04 PRIOR PILING DATE: 1999-08-04 PRIOR FILING DATE: 1999-08-04 NUMBER: OF SED ID NOS: 3 SOFTWARE: PATCHTI VAT 2 1	216 RT M: Saccharomyces c 53-3	Query Match Best Local Similarity 25.0%; Score 118.5; DB 4; Length 216; Best Local Similarity 25.0%; Pred. No. 0.00097; Matches 54; Conservative 37; Mismatches 80; Indels 45; Gaps 11; Qy 250 GKFQVVAIEGLDATGKTTVTQSVADSLK-AVLLKSPPSCIGGWRKIFDDEFTI 301	3 GRGKLILIEGLDRTGKTTQCNILYKKLQPNCKLLKFPERSTRIGGLINEYLTDDSFQL 302 IRRAFYSLGNYIVASEIAKESAKSP-VIVDRYWHSTATYAIATEVSGGLQHLPPAHH :	DD 8.1 SDQAIHDLFSANKWELVDKIKKUDLBGKNIVMDKYVSGVAXSAKGING 110 QY 358 PVYQWPE-DILKPDLILLIVVSPERRLQRLQGRGMEKTREEAELEANSVFRQKVEMS 413	Qy 414 YQRMENPGCHVVDASPSREKVLQTVLSLI 442 : : : : Db 164 FMKLLDKEIRKGDESITIVDVTNKGIQEVEALI 196	RESULT 7 US-09-252-991A-25690 ; Sequence 25690, Application US/09252991A ; Patent No. 6551795;	JAPPLICANT: MARC J. Rubenfield et al. JITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS J. TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS J. FILE REFERENCE: 107196.136
Db 1 BCTSFIPEARAVLDLVDQCPKQIQKGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSP 60 QV 285 284	61 CTSFIPEARAVLDLVDQCPKQKGKFQVAIEGLDATGKTTTQQCTSFIPEARAVLDLVDQC 285PSCIGGWRKIFDDRPTIR	121 PKEVQKGKEQVIAIEGLDATGKTTLTQHFKSLSRLSSYSRHPSCIGQWRKIFDDEPTIIR 1	Qy 304 RAPYSLGYYIVASBIAKESAKS325 	326	DD	AELEANSV 405 	RESULT 5 US-09-252-91A-28002 ; Sequence 28002, Application US/09252991A ; Patent No. 6551795 ; GENERAL INFORMATION: ; APPLICANT: Marc J. Rubenfield et al. ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS ; TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS ; FILE REPERENCE: 107196,136	TION DATE: ON NU TE: ON NU	FALOK FILLING DATE: 1998-0/-2/ NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 28002 LENGTH: 956 TYPE: PRT ORGANISM: Pseudomonas aeruginosa	US-09-252-991A-28002 Query Match Sest Local Similarity 22.4%; Pred. No. 0.00076; Matches 124; Conservative 55; Mismatches 182; Indels 193; Gaps 29;	יט רט +	310 REDAPGLARRPPAQQGPPAG	Db 370 PERLRQQLLPGPGTRHRHRLGAGRGPLRFDPRPTVRQPAAGHAHIRGEHLHACGDS 425 Qy 157 PRPHLGEFBADPRGQLMQRLWBVQDGRRLQVGCAQVVPVPEPPLHPV 203 Db 426 RARPRATDPGPLARPBGAAGKPPDPAGTRIGHTBGTFTTGTCAGDDDDDDDD 400	204 VPDLPS

10;

Gaps

41;

Indels

Length 213;

5.0%; Score 117.5; DB 4; 23.6%; Pred. No. 0.0012; Mismatches 85;

42; Mismatches

Conservative

52;

---AVLLKSPP-

255 VAIEGLDATGKTTVTQSVADSLK---

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392 RSKDIMLAAWLGEAW--LORGGLGGLGRALVLLAELCERYPEEVHPOAODGDOSWRVPPI 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 APGDADAPDPRLAALLGPPERSYSLCVPVTPDAGC~-GARVRAARLHQRLLHQLRRGPFQ 108
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TITLE OF INVENTION: Crystallization and Structure Determination of
TITLE OF INVENTION: Crystallization and Structure Determination of
TITLE OF INVENTION: Staphylococcus Aureus Thymidylate Kinase
FILE REPERBUCE: 6245.NCP
CURRENT APPLICATION NUMBER: US/09/632,553
CURRENT FILING DATE: 2000-08-04
PRIOR FILING DATE: 1999-08-04
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                                                                                                                                                                                                                                                                                                                                    5.0%; Score 118; DB 4; Length 681;
llarity 23.2%; Pred. No. 0.0067;
Conservative 49; Mismatches 189; Indels 17
CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR PILING DATE: 1998-07-27
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Patent No. 6689595
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
                                                                                                                                                     NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25690
LENGTH: 681
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Best Local Similarity
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US-09-632-553-2
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US-09-252-991A-24254

US-09-252-991A-24254, Application US/09252991A

Sequence 24254, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERBNCE: 107196.136
Sequence 7540, Application US/09489039A

Sequence 7540, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US/09/489,039A

PRIOR PRILING DATE: 1999-01-27

PRIOR PRILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
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22.1%; Pred. No. 0.0013;
iive 41; Mismatches 85;
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US-09-489-039A-7540
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TYPE: PRT ORGANISM: Escherichia coli

LENGTH: 213

NUMBER OF SEQ ID NOS: SOFTWARE: PatentIn Ve

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Best Local Similarity
JS-09-632-553-2
           Query Match
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QHLPPAHHPVYQWPEDLLKPDLILLTTVSPEBRLQRLQGRGMEKTREEAELEANSVFRQK 409
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                                                              177 WEVQDGRRLQVGCAQVVPVPEPPLHPVVPDLPSSVVFPDREAARAVLEECTSFIPEARAV
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                                                                                                      --PALAALGDPQAA-
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                                                                                                                                                                                                                                                                                                                                                                                               410 VEMSYQRMENPGCHVVDASPSREKVLQTVLSLIQ 443
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APPLICANT: Zalacain, Magdalena
APPLICANT: Zalacain, Magdalena
APPLICANT: Zalacain, Magdalena
APPLICANT: Chalker, Alison F.
APPLICANT: Ingraham, Karen A.
APPLICANT: Traini, Christopher M.
APPLICANT: Warren, Patrick V.
TITLE OF INVENTION: tdk
FILE REFERENCE: GM10201
CURRENT APPLICATION NUMBER: US/09/259,109
CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6270762
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Best Local Similarity
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US-09-583-110-5141
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LENGTH: 212
TYPE: PRT
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US-09-259-109-2
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Sequence 25642, Application US/09252991A
Patent No. 655195
GENERAL INFORMATION:
TYPE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILLING DATE: 1998-02-18
PRIOR FILLING DATE: 1998-02-18
PRIOR FILLING DATE: 1998-02-18
PRIOR FILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---AWEEDAVVDALCAA-- 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQAGGAQQGFLLRDPLDDPDTRQALLELLGACQE--APR---PHLGEFEADPRGQLWQRL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LGPPERSYSLCVPVTPDAGCGARVRAARLHQRLLHQLRRGPFQRCQLLRLLCYCPG 121
                                                                                                                                                                                                                                                                                                                                                                                                   765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    766 DHGAGLGCEPGPAPGPA-APLPPRQRLRMAVGRAAGNLGHRGKRTALPPRPGTQPEHRAI 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 SLCVPVTPDAGCGA----RVRAARLHORLL---HOLRRGPFORCOLLRLLCYCPGGOAG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 GAQQGFLLRDPLDDPDTRQALLELLGACQEAPRPHLGEFEADPRGQLWQRLWEVQDGRRL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SPPERPRPGEL---PRPRTVQVLGQAAQARPV 912
                                                                                                                                                                                                                                                                                                                                                            41
                                                                                                                                                                                                                                                                                                                                                                                                                                            73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- PGGOPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 RLLRGPLSGPLLGRRGVCAGAMAPPCRFVLELPDCTLAHFALGADAPGDADAPDPRLAAL
                                                                                                                                                                                                                                                                                                                                                                                                     706 ARRAVPGAGGDPPSVPWSRPLLAGPGTIDRGLAAGRPAGDSVQGAAAGGTGGLASDPGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                            -- PPERSY
                                                                                                                                                                                                                                                                                                                                                            -GAMAPPCRFVLELPDCT
                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                      92;
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                                                                                                                                                                                                                                                                           DB 4; Length 955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                      83;
                                                                                                                                                                                                                                                                                                                                                                                                                                              -RLAALLG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170;
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                                                                                                                                                                                                                                                                             ; Score 109; DB 4;
; Pred. No. 0.094;
14; Mismatches 8
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        CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24254
          APPLICATION NUMBER: US/09/252,991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 QVGCAQVVPVPEPPLHPVVPDLP 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    913 RPGDRRSAELPERQLRP-DPGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                              LAHFALGAD ---APGDADAPDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
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                                                                                                                                                                                                                   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                               4.6%;
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                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
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US-09-252-991A-25642
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                                                                                                                                                                                                TYPE: PRT
ORGANISM:
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Matches
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Patent No. 655177 Application US/0925291A

Patent No. 655177 Application US/0925291A

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 GQLWQRLWEVQDGRRLQVGCAQVVPVPEPPLHPVVPDLPSSVVFPDREAAR-AVLEECTS 228
                                             116 LCYCPGGQAGG--AQQGFLLRDPLDDPDTRQALLELLGACQEAP--RPHLGEFEADPRGQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 FIPEARAVLD--LVDQCPKQIQKGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPS 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 CIGOWRKIFDDEPTIIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVS 346
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                                                                                         ---AORLLHLPRLSRGVPHROPOPGRHHR---RGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 ARRILIRGPLSGPLLGRRGVCAGAMAPPCRFVLELPDCTLAHFALG-----ADAPGDADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GR-----PADHPDHRAAVDLRRAAAGAGLRDDEHLYADRPGHPDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      822 POQQARHPHGRVRQRTATPRAPRPPRGDPARRADPPAAGADDHRGNGLRPGAAALRQR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           934 RSAGEQGMKRSYPNLSRLALALAVGTGLAACSVGPDYQRPQSPPPRVASEHLGEFSGERR
                                                                                                                                                                    Gaps
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                                                                                                                                       172 LWQRLWEVQDGRRLQVGCAQVVPVPEPPLHPVVPDLPSSVVFPDRBAARAVLEEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Mismatches 189; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1026 NLRSARALFDDRWLDQLPQVTSQAGYSRSIEQQLDYDGEP--RRRLAESYRA-
  -AGLRPGQAAEAAQGRARLPHQRRRRP-
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                                                                                              -----RRAAGVRAQERQAAHRP
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Matches 113; Conservative
1530 PAPPVAATAGGA-
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                                                                                                                                                                                                                                                        RESULT 15
US-09-252-991A-20577
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ORGANISM:
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                        APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MAIC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PLICATION NUMBER: US 60/074,788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATY----AIATEVSGGLQHLPP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELLLYIASRRQHLVEKVLPALEAGKLVIMDRFIDSSVAYQGFGRGLDIEAIDWLN---- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 AHHPVYQWPEDLLKPDLILLLTVSPEBRLQRLQGRGMEKTREEABLEANSV-FRQKVEMS 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
4.5%; Score 107; DB 4; Length 212;
Best Local Similarity 24.5%; Pred. No. 0.014;
Matches 52; Conservative 34; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 VVAIEGLDATGKTTVTQSVADSLK----AVLLKSPPSCIGQWRKIFD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 YLSLLDKEGNRIVKIDASLPLEQVVETTKAVL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 Y-QRMENPGCHVV--DASPSREKVLQTVLSLI 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                      CURRENT APPLICATION NUMBER: US/99/583,110
CURRENT APPLICATION NUMBER: US/99/583,110
PRIOR APPLICATION NUMBER: US/99/583,110
PRIOR PILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR PLICATION NUMBER: US/90/85,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US/90/51,553
PRIOR PILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMBER: US 60/074,788
1998-02-18
IMBER: US 60/094,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17231, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-07
NUMBER OF SEQ ID NOS: 3314
SEQ ID NO 17231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SULT 14
-09-252-991A-17231
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                                                                                                                                                                                                                                                                                                                            SEQ ID NO 5141
LENGTH: 212
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Search completed: October 22, 2004, 23:33:21 Job time: 32 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 22, 2004, 20:24:38; Search time 116 Seconds (without alignments) 1388.530 Million cell updates/sec Run on:

US-10-681-223-2 2362 1 MAFARRILRGPLSGPLLGRR.....SREKVLQTVLSLIQNSFSEP 449

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 Total number of hits satisfying chosen parameters:

2002273 seqs, 358729299 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2001s:*

7: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ن			SUMMAKIES	
	Score	Query Match	Length	DB	ID	Description
1	2362	100.0	449	9	ABU08678	Abu08678 Novel hum
7	2362	100.0	449	7	ADC63370	Adc63370 Human nov
m	2362	100.0	449	œ	ADN49356	Adn49356 Human kin
4	2350	99.5	449	7	AAE38613	Aae38613 Human thy
Ŋ	2350	99.5	449	œ	ADI40851	Adi40851 Human kin
9	2350	99.5	449	œ	ADP84606	Adp84606 Human bre
7	2177.5	92.2	422	7	ADC39136	
00	2177.5	92.2	422	80	ADH42559	Adh42559 Novel hum
6	1552	65.7	395	7	AAE38614	Aae38614 Mouse thy
10	1552	65.7	395	œ	ADJ76250	Adj76250 Marker ge
11	1185	50.2	251	7	ADC39138	Novel h
12	1185	50.2	251	8	ADH42565	Adh42565 Novel hum
13	1137	48.1	290	7	ADF76971	Adf76971 Novel hum
14	982.5	4	200	æ	ADH42561	Adh42561 Novel hum
15	982.5		200	œ	ADH42563	Adh42563 Novel hum
16	795.5	m	508	7	ADC63372	Adc63372 Mouse thy
17	795.5	33.7	508	ω	ADN49358	Adn49358 Mouse thy
18	677.5	7	431	S	ABB57297	Abb57297 Mouse isc
19	140		243	9	ABU39443	Abu39443 Protein e
	137.5	5.8	9	M	AAG20877	Aag20877 Arabidops
	132		0	œ	ADN47368	Adn47368 Thermococ
	131.5		0	9	ABU25993	Abu25993 Protein e
23	129.5	5.5	926	7	AB079256	
	128.5	5.4	$^{\circ}$	'n	AAG20878	
25	128.5	5.4	224	m	AAG50881	Aag50881 Arabidops

Aag50880 Arabidops	Aab96152 Putative	Aay28787 E.coli th	Aau35434 Haemophil	Abu30252 Protein e	Adj62328 H influen	Abu33667 Protein e	Abu49446 Protein e	Aar07563 Polypepti	Aay28793 Schizosac	Abu22243 Protein e	Aay28785 Thymidyla	Aay28794 Thymidyla	Aay28789 Thymidyla	Aay28796 Yeast thy	Aab72202 S. cerevi	Adj62330 H influen	Abo76944 Pseudomon	Aay28786 E.coli th	Aau34536 E. coli c
AAG50880	AAB96152	AAY28787	AAU35434	ABU30252	ADJ62328	ABU33667	ABU49446	AAR07563	AAY28793	ABU22243	AAY28785	AAY28794	AAY28789	AAY28796	AAB72202	ADJ62330	AB076944	AAY28786	AAU34536
m	4	7	4	9	7	9	9	~	7	9	7	7	7	7	4	7	7	7	4
263	205	210	210	210	210	212	212	227	210	206	212	204	188	216	216	210	681	213	213
5.4	5.4	5.3	5.3	5.3	5.3	5.3	5.3	5.2	5.2	5.1	5.1	5.1	5.0	5.0	5.0	5.0	5.0	5.0	2.0
	10	56	.26	126	126	125	124.5	124	123.5	120	120	19.5	18.5	118.5	18.5	118	118	17.5	17.5
128.5	127.	12	7				12		H			Н	Н	Н	-			H	~

ALIGNMENTS

RESULT 1

ABU0867 ID AE	1 78 3U08678	standard; protein; 449 AA.
X		
O X	ABU08678;	
DT	10-JUN-2003 (1	(first entry)
X		
DE	Novel human thy	Novel human thymidylate kinase subfamily kinase.
XX		
KW		se subfamily; kinase;
₹	immune response	; kinase as
MX	pharmacogenomic	s analysis; enzyme.
ΥΥ		
3 \$	HOMO Sapiens.	
YY	701	1,000/000/0000
FT	Modified-site	1720
FT		/note= "Amidation site"
FT	Modified-site	2126
FT		/note= "Myristoylation site"
FT	Modified-site	
FT		/note= "Myristoylation site"
FT	Modified-site	181184
FT		/note= "Amidation site"
FT	Modified-site	166
FT		/note= "ATP/GTP-binding site motif A (P-loop)"
FT	Modified-site	
FT		/note= "Myristoylation site"
134	Modified-Site	
FT		/note= "Protein kinase C phosphorylation site"
EI EI	Modified-site	274
FT		/note= "Casein kinase II phosphorylation site"
F	Modified-site	77.
FT		/note= "Protein kinase C phosphorylation site"
FT	Modified-site	324
FI		
FI	Modified-site	181
LH		/note= "Casein kinase II phosphorylation site"
FT	Modified-site	
FT		/note= "Myristoylation site"
FT	Modified-site	
H		/note= "Casein kinase II phosphorylation site"
LA	Modified-site	
FF		/note= "Tyrosine kinase phosphorylation site"
LA	Modified-site	148 "Garata latance III aboumbourdation
3		/note= "casein Kinase ii pnospnoryiation site"
44		

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The invention describes a new isolated nucleic acid molecule encoding a kinase of the thymidylate kinase subfamily. The human kinase polypeptides and nucleic acid molecules are useful as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins, or serve as targets for the development of human therapeutic agents that modilate kinase activity in cells and tissues that express the kinase proteins are also useful in raising antibodies or eliciting another immune response, as reagents in assays designed to quantitatively determine levels of the protein in biological fluids, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosing a disease or a predisposition to a disease mediated by the polypeptide or nucleic acid molecule, or for treating a disorder associated with the absence of, inappropriate, or unwanted expression of the protein or nucleic acid molecule. The antibodies are useful for tissue typing, in isolating or detecting kinase proteins, or in pharmacogenomic analysis. This is the amino acid sequence of the novel human thymidylate kinase subfamily kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    markers for tissues in which the corresponding protein is preferentially expressed, or in screening a compound for the ability to stimulate or inhibit interaction between the kinase protein and a molecule that normally interacts with the kinase protein. The kinase proteins and nucleic acid molecules can also be used in providing a target for
                                                                                                                                                                                                                                                                                                           New human kinase polypeptides and nucleic acid molecules, useful in the development of human therapeutic targets, or for diagnosing or treating disorder associated with the aberrant expression of the protein or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                          Difrancesco V;
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                                                                                                                                                                                                             Beasley EM,
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 2A-C; 49pp; English.
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                                                                                 31-OCT-2001; 2001US-00984880.
                                                                                                                         31-OCT-2001; 2001US-00984880.
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                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid molecule.
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N-PSDB; ABX93989.
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                                                                                                                                                                   (PEKE ) PE CORP NY.
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US6489153-B1
                                         03-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449;
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                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                      GGQAGGAQQGFILRDPLDDPDTRQALLELLGACQEAPRPHLGEFEADPRGQLWQRLWEVQ 180
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                                                                                             1 MAFARRILERGPISGPILIGREGVCAGAMAPPCRFVLELPDCTLAHFALGADAPGDADAPDP
                                                                                                                                                                                                   RLAALLGPPERSYSLCVPVTPDAGCGARVRAARLHQRLLHQLRRGPFQRCQLLRLLCYCP
                                                                                                                                                                                                                                                   61 RLAALLGPPERSYSLCVPVTPDAGCGARVRAARLHQRLLHQLRRGPFQRCQLLRLLCYCP
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                                                                                                                                                1 MAFARRLLRGPLSGPLLGRRGVCAGAMAPPCRFVLELPDCTLAHFALGADAPGDADAPDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGRRLQVGCAQVVPVPEPPLHPVVPDLPSSVVPPDREAARAVLEECTSFIPEARAVLDLV
                                                  Gaps
                                                .;
100.0%; Score 2362; DB 6; Length 449; 100.0%; Pred. No. 1.2e-230;
                                                  Indels
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The invention relates to an isolated peptide consisting of or comprising an amino acid sequence chosen from an amino acid sequence chosen from an amino acid sequence of human kinase protein (ADC63370), an allelic variant of the kinase, orthologue or fragment. Also included are an isolated antibody that selectively binds to the kinase, an isolated mucleic acid molecule encoding the kinase proteins detailed above (appearing as the cDNA, ADC63379), and gene.

ADC63371), a gene chip comprising the nucleic acids, a transgenic non-human animal comprising the nucleic acids, a moleic acid vector comprising the nucleic acids in a sample, detecting the presence of the kinase in a sample, detecting the presence of the kinase of the kinase or condition mediated by a kinase protein and identifying a disease or condition mediated by a chaman kinase protein and identifying a modulator of the expression of the kinase involves. The kinase is useful for identifying a modulator, for identifying an agent that binds to the kinase, for biological assays concleted to kinases, drug screening assays, identifying compounds that conclude that normally interaction between the kinase protein and a conclude that normally interaction between the kinase protein and a conclude that normally interaction between the kinase protein and a concluding assays to discover compounds that interact with kinase protein of conficulate or inhibit interacting a disorder characterised by an expension of the protein assays to disease states, diagnostic tools as an immunological marker for aberrant confines states, diagnostic tools as an immunological marker for aberrant confines states, diagnostic tools as an immunological marker for aberrant confines states, diagnostic tools as an immunological marker for aberrant confines the facilitating protein for facilitating protein trafficking or facilitating protein for manipulation of a protein for inhibiting protein for inhibiting protein for production, probes, primers, productions are production.
                            Novel isolated human kinase protein useful for drug screening assays, as
361 OWPEDLIKPDLILLLTVSPEERLORLOGRGMEKTREEABLEANSVFROKVEMSYQRMENP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a target for diagnosing disease, pharmacogenomic analysis, and for identifying compounds that modulate kinase activity.
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                                                                                             421 GCHVVDASPSREKVLQTVLSLIQNSFSEP
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; enzyme; kinase; chromosome 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 2; 48pp; English.
                                                                                                                                                                                                                                                          ADC63370 standard; protein; 449 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beasley EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-2002; 2002US-00277032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2001; 2001US-00984880.
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N-PSDB; ADC63369, ADC63371.
                                                                                                                                                                                                                                                                                                                                                                                           Human novel kinase protein.
                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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ADC63370
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     antigenic portions of the proteins, for determining chromosomal positions of the nucleic acid molecules, for making vectors containing the gene regulatory regions, as hybridisation probes for determining the presence, level, form and distribution of nucleic acid expression. The gene encoding the kinase is located on human chromosome 2. The present sequence represents the novel kinase.
                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                         RLAALLGPPERSYSLCVPVTPDAGGGARVRAARLHQRLLHQLRRGPFQRCQLLRLLCYCP 120
                                                                                                                                                                                             120
                                                                                                                                                                                                                GGQAGGAQQGFLLRDPLDDPDTRQALLELLGACQEAPRPHLGEFEADPRGQLWQRLWEVQ 180
                                                                                                                                                                                                                                GGQAGGAQQGGFLLRDPLDDPDTRQALLELLGACQEAPRPHLGBFBADPRGQLWQRLWEVQ 180
                                                                                                                                                                                                                                                    DGRRLQVGCAQVVPVPEPPLHPVVPDLPSSVVFPDREAARAVLEECTSFIPEARAVLDLV 240
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                                                                                                                                                                                                                                                                                                              DOCPKOIOKGKFOVVAIEGLDATGKTTVTOSVADSLKAVLLKSPPSCIGOWRKIFDDEPT
                                                                                                                                    MAFARRLLRGPLSGPLLGRRGVCAGAMAPPCRFVLELPDCTLAHFALGADAPGDADAPDP
                                                                                                                                                                                           RLAALLGPPERSYSLCVPVTPDAGCGARVRAARLHORLLHOLRRGPFORCOLLRLLCYCP
                                                                                                                                                                                                                                                                                           DQCPKQIQKGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPT
                                                                                                                                                                                                                                                                                                                                 IIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVY
                                                                                                                                                                                                                                                                                                                                                                       QWPEDLLKPDL1LLLTVSPEERLQRLQGRGMEKTREEAELEANSVFRQKVEMSYQRMENP
                                                                                                                 Gaps
 expressing
                                                                                                                6
                                                                                             Length 449;
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          response; protein therapy; human; enzyme.
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/note= "ATP/GTP-binding site motif A"
259. .264
                                                                                            100.0%; Score 2362; DB 7;
100.0%; Pred. No. 1.2e-230;
iive 0; Mismatches 0;
constructing recombinant
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|121. 126
|note= "N-myristoylation site"
|84 .184
                                                                                                                                                                                                                                                                                                                                                                                                                        GCHVVDASPSREKVLQTVLSLIQNSFSEP 449
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                                                                                                                Matches 449; Conservative
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/note= "
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 intermediates,
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                                                                                              Query Match
Best Local Similarity
                                                                            Sequence 449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinase; immune
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The present invention provides human kinase polypeptides and the encoding polynucleotides. The invention is useful in the development of human therapeutic and diagnostic compositions, to identify therapeutic proteins and serve as targets for the development of human therapeutic agents that medulate kinase activity in cells and tissues, to elicit an immune response and for diagnosing and treating disorders characterised by the absence of inappropriate and unwanted expression of the protein. The jolypeptide is also useful in protein therapy. The present sequence is the human kinase protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated human kinase proteins, useful for diagnosing or treating disorders having an absence of, inappropriate, or unwanted expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09
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note= "Protein kinase C phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Casein kinase II phosphorylation site"
                                                                                                                                                                            'note= "Protein kinase C phosphorylation site
                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Tyrosine kinase phosphorylation site"
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                                         "Protein kinase C phosphorylation
                                                                                      II phosphorylation
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Pred. No. 1.2e-230;
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"N-myristoylation site"
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                                                                                   "Casein kinase
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22-OCT-2002; 2002US-00277032.
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N-PSDB; ADN49355, ADN49357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynuclectide and its encoded thymidylate kinase (TK), useful for identifying modulators of TK activity (e.g. agonists or antagonists) that provides therapeutic effects, and in gene therapy for treating cancers.
                                                                    300
                                                                                               360
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                                                                                                                                                                              420
               240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human thymidylate kinase (TK) polypeptides (EC 2.7.4.9) and polynucleotides. TK is also referred to as ATP-dTMP phosphotransferase. TK sequences are useful for identifying test compounds, that may act as agonists or antagonists at the receptor site and which can be regulated to provide therapeutic effects. Vectors comprising TK polynucleotides are useful in the preparation of a medicament for modulating the activity of TK in a disease, particularly cancer. The invention is also useful in gene therapy. The present sequence is human thymidylate kinase protein. TK gene is located on
                                                                                                                                                                                                                                                                                                                                                                                                             thymidylate kinase; BC 2.7.4.9; ATP:dTMP phosphotransferase; TK; cancer; gene therapy; chromosome 2p25.2.
                                                              241 DQCPKQIQKGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPT
                                                                                               IIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVY
                                                                                                                   IIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVY
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25-NOV-2002; 2002US-0428711P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                enzyme; cancer;
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7; Length 449;

Score 2350; DB 7; Length 4
Pred. No. 2e-229;
); Mismatches 1; Indels

0;

99.5%;

Query Match
Best Local Similarity 99.8
Matches 448; Conservative

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human; kinase and phosphatase; KPP; enzyme; cardiovascular; antiarteriosclerotic; hypotensive; vasotropic; antiinflammatory; antianghal; anti-HIV; antiallergic; antiasthmatic; immunosuppressive; antianghal; anti-HIV; antiallergic; antiasthmatic; immunosuppressive; antityroid; dermatological; antidabetic; nephrotropic; antigout; ophthalmological; antihermatic; antiparthic; antiarthritic; uropathic; ophthalmological; antihermatic; antipsoriatic; hemostatic; ovrostatic; antihaematic; antipsoriatic; hemostatic; ovrostatic; antihaematic; antipsoriatic; hemostatic; virotide; protozoacide; fungicide; gene therapy; kinase modulator; phosphatase modulator; growth and development disorder; growth and development disorder; ell proliferative disorder; infection.
                                                                                                 61 RIAALLGPPERSYSLCVPVTPDAGGGARVRAARLHQRLLHQLKLHQFRCPFQRCQLLRLLCYCP 120
                                                                                                                                                                                      GGQAGGAQQGFLLRDPLDDPDTRQALLELLGACQEAPRPHLGEFFADFRGQLWQRLWEVQ 180
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                              1 MAFARRILRGPLSGPLLGRRGVCAGAMAPPRRFYLELPDCTLAHFALGADAPGDADDP
                                                                           RLAALLGPPERSYSLCVPVTPDAGCGARVRAARLHQRLLHQLRRGPFQRCQLLRLLCYCP
                                                                                                                                                                                                                                 DGRRLQVGCAQVVPVPEPPLHPVVPDLPSSVVFPDREAARAVLEECTSFIPEARAVLDLV
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MAFARRILIRGPLSGPLLGRRGVCAGAMAPPCRFVLELPDCTLAHFALGADAPGDAPDP
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02-AUG-2002; 2002US-0400509P.
02-AUG-2002; 2002US-0400783P.
15-AUG-2002; 2002US-0404027P.
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Sun Oct 24 15:19:29 2004

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The present sequence represents a human kinase and phosphatase (KPP)

protein KPP sequences have cardiovascular, antiatreriosclerotic,

protein kPP sequences have cardiovascular, antiathyroid,

antiallergic, antiasthmatic, immunosuppressive, antithyroid,

dermatological, antidabetic, nephrotropic, antigout, gastrointestinal,

cantinheumatic, antiparkinsonian, nootropic, antigout, gastrointestinal,

cantiheumatic, antiparkinsonian, nootropic, antigout, peptchalmological,

antiparciatic, heemostatic, rytostatic, antilipaemic, antiparasitic,

cus, antiparciatic, heemostatic, rytostatic, antilipaemic, antiparasitic,

cus, antiparciatic, heemostatic, rytostatic, antilipaemic, antiparasitic,

cus, antiparciatic, heemostatic, rytostatic, antilipaemic, antipares and

antichlminthic, antibacterial, virucide, protozoacide and fungicide

cutivities, and can be used for diagnosing, treating or preventing disorders

conclusions and person expression of KPP, such as cardiovascular

associated with aberrant expression of KPP, such as cardiovascular

ciseases (e.g. atherosolerosis, hypertension, vasculitis, cronvic

diseases (e.g. atherosolerosis, proteins), contact dermatitis, Crohn's

ciseases (e.g. atherosolerosis, proteins), or vasculitis, contact

disease, diabetes melliture), immune system disorders (e.g. ADS,

allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's

disease, diabetes melliture), immune system disorders (e.g. Alzheimer's

contective tristis, neurological disorders (e.g. Alzheimer's

costeoporosis, pancreatitis, neurological disorders (e.g. Alzheimer's

costeoporosis, parkence, ruseue disease, dementia or

cepilepsy), disorders affecting growth and development (e.g. cirrhosis,

contective anticological and disorders (e.g.

compounds on the expression of multiple contective, or viral, bacterial,

contective and and development of the expression of molect acids and kinases and

polymucleotides are also useful in assessing the effect of expendence or polymucleotides encoding KPP are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DQCPKQIQKGKEQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RLAALLGPPERSYSLCVPVTPDAGCGARVRAARLHQRLHQLRRGPFQRCQLLRLLCYCP 120
                                                                                                                                                                                                         New human kinases and phosphatases, useful for diagnosing, treating or preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAFARRLLRGPLSGPLLGRRGVCAGAMAPPRRFVLELPDCTLAHFALGADAPGDADAPDP
Khare R;
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                                                                Lee
            Baughn MR, Tang YT, Lal PG, Lee SY, Griffin JA, Khare R;
Elliott VS, Jin P, Hawkins PR, Swarnakar A, Chawla NK, Tran
Guruzajan R, Ding L, Marquis JP, Thornton MB, Forsythe IJ, I
Gietzen KJ, Ramkumar J;
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Pred. No. 2e-229;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 17; 330pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to model human disease.
                                                                                                                                      2004-132950/13.
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                                                                                                                                                               N-PSDB; ADI40904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 449 AA;
                                                                                                                                                                                                                                                           sclerosis, os
or hepatitis
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ô 120 420 RLAALLGPPERSYSLCVPVTPDAGCGARVRAARLHQRLLHQLRRGPFQRCQLLRLLCYCP 120 GGQAGGAQQGFLLRDPLDDPDTRQALLELLGACQEAPRPHLGEFEADPRGQLWQRLWEVQ 180 The invention comprises the amino acid and coding sequences of human breast-specific proteins. The DNA and protein sequences of the invention are useful for the diagnosis, treatment and prevention of breast cancer. The present amino acid sequence represents a human breast-specific 09 09 useful for 1 MAFARRILRGPLSGPLLGRRGVCAGAMAPPRRFVLELPDCTLAHFALGADAPGDADAPDP 61 RLAALLGPPERSYSLCVPVTPDAGCGARVRAARLHQRLLHQLRRGPFQRCQLLRLLCYCP IIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVY 301 IIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVY 1 MAFARRIIRGPISGPLIGRRGVCAGAMAPPCRFVLELPDCTLAHFALGADAPGDADAPDP Gaps New breast specific nucleic acid molecules and polypeptides usef diagnosing, preventing or treating breast cancer, for producing transgenic animals or cells, or for research purposes. .; Length 449; Indels Σ Rodriquez 1; DB 8; Score 2350; DB 8, Pred. No. 2e-229; 0; Mismatches 1 human; breast-specific protein; breast cancer. 421 GCHVVDASPSREKVLOTVLSLIONSFSEP 449 GCHVVDASPSREKVLQTVLSLIQNSFSEP 449 SEQ ID NO 205; 521pp; English Chen H, Human breast-specific protein #110. ADP84606 standard; protein; 449 Sun Y, 05-DEC-2003; 2003WO-US038815. 05-DEC-2002; 2002US-0431123P. 99.5%; (first entry) protein of the invention. 448; Conservative Turner LR, (DIAD-) DIADEXUS INC. 2004-468848/44. Query Match Best Local Similarity Sequence 449 AA; N-PSDB; ADP84474 WO2004053077-A2. Homo sapiens. 09-SEP-2004 24-JUN-2004. Macina RA, Claim 12; ADP84606; 61 121 361 421 Matches ADP84606 g g dd q q ð à ò $\stackrel{>}{\circ}$ ð ö 240 09 09 EA;

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                                                                                                                                                                                                                                                                                         nootropic, neuroprotective, immunostimulant, antiparkinsonian; anti-HIV; antiasthmatic, antinflammatory, hypotensive, antiarteriosclerotic; hemostatic; osteopathic; gene therapy,; NOVX; diabetes; obesity; cancer; lymphoma; uterus cancer; prostate cancer; dyslipidemia; anorexia; wasting disorder; Alzheimer's disease; Parkinson's disorder; cachexia; cardiomyopathy; AlDS; asthma; Crohn's disease; multiple sclerosis; hypotension; atherosclerosis; hemophilia; graft-versus-host disease;
DGRRLQVGCAQVVPVPEPPLHPVVPDLPSSVVFPDREAARAVLEECTSFIPEARAVLDLV
                                    DOCPKOLOKGKFOVVALEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGGWRKIFDDEPT
                                                                       IIRRAFYSLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVY
                                                                                  361 QWPEDLLKPDLILLIVSPEERLQRLQGRGMEKTREEABLEANSVFRQKVEMSYQRMENP
                                               QWPEDLLKFDL1LLLTVSPEERLQRLQGRGMEKTREEAELEANSVFRQKVEMSYQRMENP
          antidiabetic; cytostatic; immunomodulator; anorectic; antilipemic;
                                                                                                                                                                                                                                                                  SEQ ID NO: 78
                                                                                                                                              GCHVVDASPSREKVLQTVLSLIQNSFSEP 449
                                                                                                                                                               421 GCHVVDASPSREKVLQTVLSLIQNSFSEP 449
                                                                                                                                                                                                                                                                                                                                                          Albright hereditary osteodystrophy.
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                                                                                                                                                                                                            ADC39136 standard; protein; 422
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2001US-02883087P.
2001US-0289817P.
2001US-0299818P.
2001US-0290194P.
2001US-0290131P.
2001US-0291181P.
2001US-0291181P.
2001US-0292174P.
2001US-0292374P.
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2001US-0312270P.
2001US-0313416P.
2001US-0318463P.
2001US-0325683P.
                                                                                                                                                                                                                                                                 Novel human NOVX polypeptide
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2001US-0293747P.
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2001US-0294110P.
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2001US-0304879P.
                                                                                                                                                                                                                                                (first entry)
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15-MAY-2001;
16-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MAY-2001;
-MAY-2001;
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-MAY-2001;
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27-SEP-2001;
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11-MAY-2001;
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21-MAY-2001;
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25-MAY-2001;
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ARVRAARLHQRLLHQLRRGPFQRCQLLRLLCYCPGGQAGGAQQGFLLRDPLDDPDTRQAL 146

27 MAPPCRFVLELPDCTLAHFALGADAPGDADAPDPRLAALLGPPERSYSLCVPVTPDAGCG

Н 87 ARVRAARLHQRILHQLRRGPFQRCQLLRLLCYCPGGQAGGAQQGFLLRDPLDDPDTRQAL

121 LELLGACQEAPRPHLGEFEADPRGQLWQRLWEVQDGRRLQVGCAQVVPVPEPPLHPVVPD 180

LPSSVVFPDREAARAVLEECTSFIPEARAVLDLVDQCPKQIQKGKFQVVAIEGLDAT-GK LPSSVVFPDREAARAVLEECTSFIPBARAVLDLVDQCPKQIQKGKFQVVAIEGLDATGGK TTVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPTLIRRAFYSLGNYIVASEIAKESAKS

LELLGACQEAPRPHLGEFEADPRGQLWQRLWEVQDGRRLQVGCAQVVPVPEPPLHPVVPD

147

207 181 266

61

PUIVDRXWHSTATYALATEVSGGLQHLPPAHHPVYQWPEDLLKPDLILLLTVSPERLOR 385

TTVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPTIIRRAFYSLGNYIVASEIAKBSAKS

241 326

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which Nova polypepide. The Nova polypepide is particularly user in the Nova treating, preventing or alleviating pathology associated with Nova polypeptide in a mammal, e.g. a human. The Nova mucleic acid and polypeptide are especially useful for treating or preventing e.g. disbetes, obesity, cancers (e.g. lymphoma, uterus cancer or prostate cancer), dyslipidemias, anorexia, wasting disorders, Alzheimer's disease, darkinson's disorder, cachexia, cardiomyopathy, AIDS, astima, Crohn's graft-versus-host disease or Albright hereditary osteodystrophy. The DNA encoding the protein is useful in gene therapy for treating the above conditions. These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to new isolated NOVX polypeptides, the genes encoding them or sequences having at least 95% identity to the amino acid or nucleotide sequences. The NOVX polypeptide is useful as a therapeutic, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide. The NOVX polypeptide is particularly useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                Zhong
                                                                                                                                                                                                                                                                                                                                                                 BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      applications. This sequence represents one of the NOVX proteins of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New NOVX polypeptides and polynucleotides, useful in gene therapy, particularly for treating or preventing a syndrome associated with human disease e.g. diabetes, obesity, cancer, Alzheimer's disease, hypertension or hemophilia.
                                                                                                                                                                                                                                                                                                                                                                 Zerhusen
                                                                                                                                                                                                                                                                                                                            Kekuda R, Malyankar UM, Li L, Pena CEA, Spytek KA;
Suo X, Fernandes ER, Smithson G, Stone DJ, Zerhusen
M, Anderson DW, Mezes P. Peyman JA, Macdougall JK;
Rastelli L, Shenoy SG, Gerlach VL, Shimkets RA, Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 78; 748pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Shenoy SG,
18-OCT-2001, 2001US-0330292P.
28-NOV-2001, 2001US-033873P.
03-DEC-2001, 2001US-0337552P.
21-FEB-2002, 2002US-0359245P.
01-MAY-2002, 2002US-00136826.
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99.1%;
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Gorman L., Guo X, Fernandes
Patturalan M, Anderson DW,
Padigaru M, Rastelli L, S.
RAinger SR, Ellerman K;
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                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
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N-PSDB; ADC39135.
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                                                                                                                                                                                                                                                                                                                            Miller CE,
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301 PVIVDR--HSTATYAIATEVSGGLQHLPPAHHPVYQWPEDLLKPDLILLLTVSPEERLQR 358
                  445
                               359 LQGRGMEKTREEAELEANSVFRQKVEMSYQRMENPGCHVVDASPSREKVLQTVLSLIQNS 418
                                                                                                                                                                                      cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
                                                                                                                                                                                              antidiabetic; immunosuppressive; anti-HĪV; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; antiinfertility; cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS; multiple sclerosis; graft-versue-hors disease; Alzheimer's disease; Parkinson's disease; asthma; fertility disorder; chromosome mapping; tissue typing; preventive medicine; pharmacogenomic; vaccine.
                  LQGRGMEKTREEAELEANSVFRQKVEMSYQRMENPGCHVVDASPSREKVLQTVLSLIQNS
                                                                                                                ADH42559 standard; protein; 422 AA.
                                                                                                                                                                                                                                                                                                                                                       05-UN-2002; 2002US-0386745P.
06-UN-2002; 2002US-038635P.
06-UN-2002; 2002US-038645P.
06-UN-2002; 2002US-038645P.
06-UN-2002; 2002US-0386465P.
06-UN-2002; 2002US-0386465P.
07-UN-2002; 2002US-0386465P.
07-UN-2002; 2002US-0386701P.
07-UN-2002; 2002US-038670P.
07-UN-2002; 2002US-038670FP.
07-UN-2002; 2002US-038708P.
10-UN-2002; 2002US-038708P.
10-UN-2002; 2002US-038708P.
10-UN-2002; 2002US-038708P.
10-UN-2002; 2002US-0387640P.
11-UN-2002; 2002US-038766P.
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2002US-0385755P.
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2002US-0387668P.
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2002US-0389742P
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                                                                                                                                                                    Novel human protein NOV78a
                                                                                                                                                   (first entry)
                                                    FSEP 449
                                                                     FSEP 422
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11-JUN-2002; 2
11-JUN-2002; 2
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12-JUN-2002;
                                                                                                                                                   25-MAR-2004
                                                                                                                                                                                                                                                            Homo sapiens.
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17-JUN-2002;
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The invention relates to 566 new isolated human polypeptides and their encoding genes, sequences that are at least 954 identical to these or sequences comprising one or more conservative substitutions in these. The polypeptide, polypurelectide and antibodies against the polypeptides are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, allaheimer's disease, AlDS, multiple sclerosis, graft-versus-host disease, Alzheimer's disease, parxinson's disease, asthma, or fertility disorders. The mucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The example of the polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 ARVRAARLHQRLLHQLRRGPFQRCQLLRLLCYCPGGQAGGAQQGFLLRDPLDDPDTRQAL 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New NOVX polypeptides and nucleic acid molecules useful for preventing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL; Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR; Bilerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L; Grosse WM, Gunther E, Guo X, Gusev VV, Herrmann JL, Ji W, Kekuda F Khramtsov NV, Larochelle WJ, Li L, Liang H, Low K, Maddougall JR; Maclachlan T, Malyankar UM, Mcqueeney K, Mezick AJ, Miller CE; Millet I, Padigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L; Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G; Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ; Wolenc AR, Zhong M, Zhong H;
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2002US-0412955P.
2002US-0415195P.
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2002US-0402268P.
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2002US-0403458P.
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2002US-0403732P.
2002US-0406182P.
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19-JUN-2002; 29-JUN-2002; 29-JUN-2002; 25-JUN-2002; 20-AUG-2002; 20-AUG-2002; 213-AUG-2002; 213-AUG-2002; 20-AUG-2002; 20-
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26-AUG-2002;
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13-SEP-2002;
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30-SEP-2002;
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New polynucleotide and its encoded thymidylate kinase (TK), useful for identifying modulators of TK activity (e.g. agonists or antagonists) that provides therapeutic effects, and in gene therapy for treating cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thymidylate kinase; EC 2.7.4.9; ATP:dTMP phosphotransferase; TK;
                          LEILGACQEAPRPHLGEFEADPRGQLWQRLWEVQDGRRLQVGCAQVVPVPBPPLHPVVPD
                                                                                                                                                                                                                                 301 PVIVDR--HSTATYALATEVSGGLQHLPPAHHPVYQWPEDLLKPDLILLTVSPEERLQR
                                                                                                                                                                                                                                                                                                     LOGICOMENTREBAELBANSVFROKVEMSYQRMENPGCHVVDASPSREKVLQTVLSLIQNS
LELLGACQEAPRPHLGEFEADPRGQLWQRLWEVQDGRRLQVGCAQVVPVPRPPLHPVVPD
                                                                                                                                    TTVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPTIIRRAFYSLGNYIVASEIAKESAKS
                                                                                                                                                                    TTVTQSVADSLKAVLLKSPPSCIGOWRKIFDDEPTIIRRAFYSLGNYIVASEIAKESAKS
                                                                                                                                                                                                                                                                          LOGRIGMEKTREEAELEANSVFROKVEMSYORMENPGCHVVDASPSREKVLQTVLSLIQNS
                                                                    LPSSVVFPDREAARAVLEECTSFIPEARAVLDLVDQCPKQIQKGKFQVVAIEGLDAT-GK
                                                                                                  181 LPSSVVFPDREAARAVLEECTSFIPEARAVLDLVDQCPKQIQKGKFQVVAIEGLDATGGK
                                                                                                                                                                                                        PVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVYQWPEDLLKPDLILLLTVSPEERLQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE38614 standard; protein; 395 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse thymidylate kinase protein.
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25-NOV-2002; 2002US-0428711P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a method of testing for bronchial asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bronchial asthma, chronic obstructive pulmonary disease, respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
                                                                                                              QKGKFQVVAIBGLDAIGKITVTQSVADSLKAVILKSPPSCIGGWRKIFDDEFIIIRRAFY
                                                PPERSYSLCVPVTPDAGCGARVRAARLHQRLLHQLRRGPFQRCQLLRLLCYCPGGQAGGA
                                                              128 QQGFLLRDPLDDPDTRQALLELLGACQEAPRPHIGEFEADPRGQLWQRLWEVQDGRRLQV
                                                                                                                                               GCAQVVPVPEPPLHPVVPDLPSSVVPPDREAARAVLEECTSFIPEARAVLDLVDQCPKQI
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 Length 395;
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                          48;
65.7%; Score 1552; DB 7; 77.8%; Pred. No. 2.2e-148;
                         36; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  claim 16; SEQ ID NO 1502; 241pp; English.
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2003JP-00077212.
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                         294; Conservative
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 Query Match
Best Local Similarity
Matches 294; Conserv
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20-MAR-2003;
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contermining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the capression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthema or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13, or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (1) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polynucleotide that suppresses the compound; a protein encoded by a marker gene; and (7) a DNA chip for testing for probe has been immobilised to assay a marker gene. (1) has respiratory expression of the gene through an RNA ieffect or an antibachmatic activities, and can be used in gene therapy. The method is useful for testing for researching for the probe has been immobilised to severe there is no be used in gene therapy. The method is useful for testing for the problem or a chronic obstructive pulmonary disease, on which a problem is as the control or severe specification or a subject or an antibody recognising the control of the gene through an end antibuted to a portion of the gene through an end and be used in gene therapy. The method is useful for testing for the problem is a proportion or the problem or an antibuted or an antibuted or an antibute of the problem or an antibuted or as a portion or and antisathmatic acti and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention. chronic obstructive pulmonary disease. The method comprises 8X3999999999999999999999999999999

Sequence 395 AA;

0 68 PPERSYSLCVPVTFDAGCGARVRAARLHQRLLHQLRRGPFQRCQLLRLLCYCPGGQAGGA 127 QQGFLLRDPLDDPDTRQALLELLGACQEAPRPHLGEFEADPRGQLWQRLWEVQDGRRLQV 187 GCAQUVPVPEPPLHPVVPDLPSSVVFPDREAARAVLEECTSFIPEARAVLDLVDQCPKQI 247 QKGKFQVVAIEGLDATGKTTVTQSVADSLKAVLLKSPPSCIGOWRKIFDDEPTIIRRAFY 307 SLGNYIVASEIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVYQWPEDLL 367 256 SLGNYLVASEIAKESTNFPVIVDRYWHSTATYAIATEVSGGLQYLPPAHHPVYQWPGDLL 315 368 KPDLILLLTVSPEERLQRLQGRGMEKTREEAELEANSVFRQKVEMSYQRMENPGCHVVDA 427 316 KPDLVLLITVNSEERVRRLQGRGQEKTKEEAELEANNVFRQKVEMTYQRMENPSCHLVDA 375 75 POGAATRICVPLAPGEGCGPRVQAARVHHRLLQQLRRGPLQRCQLSKLLGYGPGDQAGEA 196 QKGKFQVIAIEGLDATGKTTLTQSVSESLKAVLLQSPPPCISQWRKIFDDEPTIIRRAFY Gaps ., Length 395; Indels 48; 65.7%; Score 1552; DB 8; 77.8%; Pred. No. 2.2e-148; 36; Mismatches 428 SPSREKVLQTVLSLIQNS 445 SPSRETVLOKVLELIOSS Matches 294; Conservative Local Similarity 376 128 94 188 248 Query Match d δ Db à Db ò g ò g ð g ò à

80.

SEQ ID NO:

Novel human NOVX polypeptide

(first entry)

18-DEC-2003

ADC39138;

ADC39138 ID ADC XX AC ADC XX DT 18-XX

AA.

ADC39138 standard; protein; 251

RESULT 11

The invention relates to new isolated NOVX polypeptides, the genes encoding them or sequences having at least 95% identity to the amino acid or nucleotide sequences. The NOVX polypeptide is useful as a therapeutic, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated Σ antidiabetic; cytostatic; immunomodulator; anorectic; antilipemic; nortropic; neuroprotective; immunostimulant; antiparkinsonian; anti-HIV; antiasthmatic; antiinflammatory; hypyotonic; antiarteriosclerotic; hemostatic; osteopathic; gene therapy, NOVX; diabetes; obesity; cancer; lymphoma; uterus cancer; prostate cancer; dyslipidemia; anorexia; cardiomyopathy; Albs; asthma; Grobn; disease; parkinson's disorder; cachexia; cardiomyopathy; Albs; asthma; Crohn; disease; multiple sclerosis; hypertension; atherosclerosis; hemophilia; graft-versus-host disease; Miller CE, Kekuda R, Malyankar UM, Li L, rena can, cristian BD; Gorman L, Guo X, Fernandes ER, Smithson G, Stone DJ, Zerhusen BD; Patturajan M, Anderson DW, Mezes PS, Peyman JA, Macdougall JR; New NOVX polypeptides and polynucleotides, useful in gene therapy, particularly for treating or preventing a syndrome associated with a human disease e.g. diabetes, obesity, cancer, Alzheimer's disease, Claim 1; SEQ ID NO 80; 748pp; English. Guo X, Fernandes ER, Smi M, Anderson DW, Mezes PS , Rastelli L, Shenoy SG, , Ellerman K; hypertension; atherosclerosis; heme Albright hereditary osteodystrophy 2001US-0288063P. 2001US-0288395P. 2001US-0289087P. 2001US-0289817P. 2001US-0290753P. 2001US-0291181P. 2001US-0291243P. 2001US-0293107P. 2001US-0293747P. 2001US-0294109P. 2001US-0294110P. 001US-0292001P. 2001US-0292374P. 2001US-0294434P. 2001US-0294827P. 2001US-0308901P. 2001US-0312270P. 2001US-0313416P. 2001US-0325683P. 2001US-0289818P 2001US-0290194P. 2001US-0304879P 2001US-0318463P 2001US-0330292P 2001US-0333873P 2001US-0336909P 2001US-0337552P 2002US-0359245P 02-MAY-2002; 2002WO-US014199 2002US-00136826 human disease e.g. diabetes hypertension or hemophilia. (CURA-) CURAGEN CORP. 2003-239445/23. N-PSDB; ADC39137 WO2003010327-A2 Homo sapiens. 15-MAY-2001; 16-MAY-2001; 18-MAY-2001; 22-MAY-2001; 23-MAY-2001; 29-MAY-2001; 29-MAY-2001; 30-MAY-2001; 31-MAY-2001; 27-SEP-2001; 28-NOV-2001; 09-MAY-2001; 14-MAY-2001; 25-MAY-2001; 12-JUL-2001; 31-JUL-2001; 18-OCT-2001; 11-MAY-2001; 17-AUG-2001; 10-SEP-2001; Padigaru M, Edinger SR, 06-FEB-2003

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WO2003102159-A2
                                                                                                                                                                                                                                                                07-JUN-2002;
07-JUN-2002;
07-JUN-2002;
polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and polypeptide are especially useful for treating or preventing each addition and polypeptide are especially useful for treating or preventing e.g. a human. The NOVX nucleic acid and diabetes, obseity, cancers (e.g. lymphoma, uterus cancer or prostate cancer), dyslipidemias, anorexia, wasting disorders, Alzheimer's disease, Parkinson's disorder, cachexia, cardiomyopathy, AlbS, asthma, Crohn's disease, multiple sclerosis, phyertension, atherosclerosis, hemophilia, graft-versus-host disease or Albright hereditary osteodystrophy. The DNA encoding the protein is useful in gene therapy for treating the above conditions. These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. This sequence represents one of the NOVX proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVTQSAADSLKAVLLKSPPSCIGGWRKIFDDEPTIIRRAFYSLGNYIVASEIAKESAKSP 128
                                                                                                                                                                                                                                                                                                                                                       87 ARVRAARLHQRLLHQLRRGPFQRCQLLRLLCYCPGGQAGGAQQGFLLRDPLDDPDTRQAL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 TVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPTIIRRAFYSLGNYIVASBIAKESAKSP 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVYQWPEDLLKPDLILLLTVSPEERLQRL 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGRGMEKTREEAELBANSVFRQKVEMSYQRMENPGCHVVDASPSREKVLQTVLSLIQNSF 446
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                                                                                                                                                                                                                                                                                               27 MAPPCRFVLELPDCTLAHFALGADAPGDADAPDPRLAALLGPPERSYSLCVPVTPDAGCG 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 LPSSVVFPDREAARAVLBECTSFIPEARAVLDLVDQCPKQIQKGKFQVVALEGLDATGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------AVLEECTSFIPEARAVLDLVDQCPKQIQKGKFQVVAIEGLDATGKT
                                                                                                                                                                                                                                                                    Indels 172; Gaps
with NOVX polypeptide. The NOVX polypeptide is particularly useful
                                                                                                                                                                                                                                          50.2%; Score 1185; DB 7; Length 251; 58.9%; Pred. No. 2.2e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue typing; preventive medicine; pharmacogenomic; vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human protein NOV78d.
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                                                                                                                                                                                                                                                                      249; Conservative
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                                                                                                                                                                                                                 Sequence 251 AA;
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                                                                                                                                                                                      nvention.
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The invention relates to 566 new isolated human polypeptides and their encoding genes, sequences that are at least 95% identical to these or sequences comprising one or more conservative substitutions in these. The polypeptide, polynucleotide and antibodies against the polypeptides are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This sequence represents an example of the polypeptide of the invention.
Padigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L; Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G; Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ; Zhong M, Zhong H;
                                                                                                                                                                                                                          treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
                                                                                                                                                                                                    nucleic acid molecules useful for preventing disorders, e.g. cancer, cardiomyopathy,
                                                                                                                                                                                                                                                                                                            Claim 2; SEQ ID NO 1118; 1503pp; English.
                                                                                                                                                                                                        and
                                                                                                                                                                                                      polypeptides
                                                                                                                                          WPI; 2004-053467/05.
                                                                                                                                                                                                                                                                     pharmacogenomics.
                                                                                                                                                               N-PSDB; ADH42564
                 Maclachlan
                                                                                                   Wolenc AR,
                                                                                                                                                                                                        NOVX
                                           Millet
                                                            Rieger
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87 ARVRAARLHQRLHQLRRGPFQRCQLLRLLCYCPGGQAGGAQQGFLLRDPLDDPDTRQAL 146 147 LELLGACQEAPRPHLGEFEADPRGQLWQRLWEVQDGRRLQVGCAQVVPVPEPPLHPVVPD 206 266 267 TVTQSVADSLKAVLLKSPPSCIGQWRKIFDDEPTIIRRAFYSLGNYIVASEIAKESAKSP 326 69 TVTQSAADSLKAVLLKSPPSCIGQWRKIFDDEPTIIRRAFYSLGNYIVASEIAKESAKSP 128 VIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVYQWPEDLLKPDLILLLTVSPEERLQRL 386 387 QGRGMEKTREEAELEANSVFRQKVEMSYQRMENPGCHVVDASPSREKVLQTVLSLIQNSF 446 189 QGRGMEKTREEABLEANSVFRQKVEMSYQRMENPGCHVVDASPSREKVLQTVLSLIQNSF 248 68 98 22 22 27 MAPPCRFVLELPDCTLAHFALGADAPGDADAPDPRLAALLGPPERSYSLCVPVTPDAGCG ----AVLEECTSFIPEARAVLDLVDQCPKQIQKGKFQVVAIEGLDATGKT 207 LPSSVVFPDREAARAVLEECTSFIPEARAVLDLVDQCPKQIQKGKFQVVAIEGLDATGKT Indels 172; Length 251; 2; Score 1185; DB 8; Pred. No. 2.2e-111; 0; Mismatches MAPPRREVLELPDCTLAHFALG 50.2%; fatches 249; Conservative Local Similarity Sequence 251 AA; 23 23 23 327 Query Match 임 à g à q ò qq δ g ð d à Dp ò

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This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular cyganisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information or ceedived from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as paramaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the CDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a current in a mammal. In addition, they may be useful for measuring or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 IAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVYQWPEDLLKPDLILLLTV 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 EGLDATCKTTVTQSVADSLKAVLLKSPPSCIGQWRKIFDDBPT1IRRAFYSLGNYIVASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New PRO polypeptides, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 PVVPDLPS-SVVFPDREAARAVLEECT---SFIPEARAVLDLVDQCPKQIQKGKFQVVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 PIWATLPSWRVSKRERAIPRRGKSLCTVYLLYIPBARAVLDLVDGCPKQIQKGKFQVVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.;
                                                                                                     human, PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; actor; actor; cytotoxic factor; differentiation factor; reuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schoenfeld JR;
                                                            Novel human secreted and transmembrane protein SeqID 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jackman JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; SEQ ID NO 646; 918pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hunte B, Wu TD;
                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2003; 2003WO-US005241.
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                    26-FEB-2004 (first entry)
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N-PSDB; ADF76970.
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es 229; Conserv
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                                                                                                                                                                                                                                                                                WO2003072035-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams PM,
                                                                                                                                                                                                                                       Homo sapiens.
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98

ADF76971 standard; protein; 290 AA

RESULT 13
ADF76971
ID ADF76
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AC ADF76

ADF76971;

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        218
                                       278
        159 IAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVYQWPEDLLKPDLILLLTV
                                 219 SPEERLQRLQGRGMEKTREEAELEANSVFRQKVEMSYQRMENPGCHVVDASPSREKVLQT
                       378 SPEERLQRLQGRGMEKTREBAELEANSVFRQKVEMSYQRMENPGCHVVDASPSREKVLQT
ADH42561 standard; protein; 200 AA.
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2002US-0387429P.
2002US-0387429P.
2002US-038766P.
2002US-038766F.
2002US-038766P.
2002US-038766P.
2002US-038766P.
2002US-0387659P.
2002US-0387659P.
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2002US-0386447P.
2002US-0386459P.
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2002US-0386931P.
2002US-0387078P.
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2002US-0387960P.
2002US-0388022P.
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2002US-0386041P.
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                                                                                                                                                           Novel human protein NOV78b.
                                                                                                                                            (first entry)
                                                                     VLSLIQNSFSEP 290
                                                        VLSLIQNSFSEP 449
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07-UUN-2002;
07-UUN-2002;
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11-JUN-2002;
11-JUN-2002;
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The invention relates to 566 new isolated human polypeptides and their encoding genes, sequences that are at least 95% identical to these or sequences comprising one or more conservative substitutions in these. The polypeptide, polymedie or more conservative substitutions in these. The useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, allaheimer's disease, AlDS, multiple sclerosis, graft-versus-host disease, Alzheimer's disease, parkinson's disease, asthma, or fertility disorders. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This sequence represents an example of the polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 ASBIAKESAKSPVIVDRYWHSTATYAIATEVSGGLQHLPPAHHPVYQWPEDLLKPDLILL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burgess CE, Casman SJ, Catterron E, Dhandol M, Edinger SR, Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L; Eckeda R, Gorsse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Tekuda R, Khramtsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR; Maclachlan T, Malyankar UM, Mcqueeney K, Mezick AJ, Miller CE; Miller I, Ratturajan M, Peyman JR, Qian X, Rastelli L; Rieger DK, Stone DM, Stone DM, Stone DM, Skeney SG, Shinkets RA, Smithson G; Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;
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treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
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al M, Edinger SR;
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99.0%; Pred. No. 6.1e-91;
iive 1; Mismatches 0;
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18-JUN-2002; 2002US-0389604P.
18-JUN-2002; 2002US-0389864P.
19-JUN-2002; 2002US-0399884P.
19-JUN-2002; 2002US-0390006P.
19-JUN-2002; 2002US-0390144P.
19-JUN-2002; 2002US-0390209P.
25-JUN-2002; 2002US-040162P.
12-AUG-2002; 2002US-040162P.
13-AUG-2002; 2002US-04018P.
15-AUG-2002; 2002US-040345P.
15-AUG-2002; 2002US-04018P.
15-AUG-2002; 2002US-0410385P.
15-AUG-2002; 2002US-0410385P.
13-SEP-2002; 2002US-0410565P.
13-SEP-2002; 2002US-0410565P.
23-CCT-2002; 2002US-0410565P.
23-CCT-2002; 2002US-0410565P.
23-CCT-2002; 2002US-0410565P.
23-CCT-2002; 2002US-0410565P.
23-CCT-2002; 2002US-042082P.
24-CCT-2002; 2002US-042082P.
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Best Local Similarity 99.0
Matches 193; Conservative
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375 LTVSPEERLORLOGRGMEKTREEAELEANSVFROKVEMSYORMENPGCHVVDASPSREKV 434
                  123 LTVSPEERLORLOGRGMEKTREEABLEANSVFRQKVEMSYQRMENPGCHVVDASPSREKV 182
                                                                                                                                                                                                                                                                                                                        tissue typing; preventive medicine; pharmacogenomic; vaccine.
                                                                                                                                       ADH42563 standard; protein; 200 AA
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11-JUN-2002; 2002US-0387668P.

11-JUN-2002; 2002US-0387659P.

11-JUN-2002; 2002US-0387859P.

12-JUN-2002; 2002US-0387934P.

12-JUN-2002; 2002US-0387960P.

12-JUN-2002; 2002US-03887960P.
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2002US-0386515P
2002US-0386355P
2002US-0386357P
2002US-0386447P
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2002US-0386447P
2002US-0386447P
2002US-038644P
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2002US-0389123P.
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2002US-0388432P.
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2002US-0389146P.
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2002US-0389604P
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                                                 LQTVLSLIQNSFSEP
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06-JUN-2002;
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07-JUN-2002; 2
07-JUN-2002; 2
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12-JUN-2002; 2
12-JUN-2002; 2
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17-JUN-2002;
18-JUN-2002;
18-JUN-2002;
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The invention relates to 566 new isolated human polypeptides and their encoding genes, sequences that are at least 954 identical to these or sequences comprising one or more conservative substitutions in these. The polypeptide, polypucleotide and antibodies against the polypeptides are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity, alzheimer's disease, halb, multiple sclerosis, graft-versus-host disease, halb, multiple sclerosis, graft-versus-host disease, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This sequence represents an example of the polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL; Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR; Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Growan L, Grosse WM, Gunther E, Guo K, Gusev VY, Herrmann JL, Ji W, Kekuda R Khramtsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR; Maclachlan T, Mayankar UM, Mcqueeney K, Mezick AJ, Miller CE, Miller I, Padigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L; Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G; Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ; Wolenc AR, Zhong M, 
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                    2002US-0390144P-
2002US-0390209P-
2002US-0390209P-
2002US-0401628P-
2002US-040268P-
2002US-040368P-
2002US-0403458P-
2002US-040341P-
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2002US-040341P-
2002US-0410385P-
2002US-0410385P-
2002US-0410385P-
2002US-0410385P-
2002US-0410385P-
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23-OCT-2002; 2002US-0420627P.
23-OCT-2002; 2002US-0420718P.
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01-NOV-2002; 2002US-0423095P.
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Matches 193; Conservative
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                       19-JUN-2002; 2
19-JUN-2002; 2
25-JUN-2002; 2
06-AUG-2002; 2
12-AUG-2002; 2
13-AUG-2002; 2
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15-AUG-2002; 2
26-AUG-2002; 2
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13-SEP-2002;
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Wolenc AR,
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375 LTVSPEERLQRLQGRGMEKTREEAELEANSVFRQKVEMSYQRMENPGCHVVDASPSREKV 434

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qq ò Search completed: October 22, 2004, 23:30:58 Job time : 123 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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BG779993	BF102537	BF243467	B1818166	BG776607	AV707941	BF242831	BG776636	BG771320	BG501398	BF242245	BG497460	BG547557	BY704814	BE748211	BF031764	BU166495	BF243749	BI918806	BG180852	BG255761
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ALIGNMENTS

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

EST: *

Database :

Score 885.2; DB 5; Length 1003; Pred. No. 3.2e-198;

34.4%;

Query Match Best Local Similarity us-10-681-223-1.rst

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BC027329.1
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Matches 1121;
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                                                 Mus musculus (house mouse)
Mus musculus
Mus musculus
Sukaryyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3124)
                                                                                                                                                                                                                           Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 36 Row: e Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hulyk, S.W., Hale, S.M.,
Martin, R.G., Muzny, D.M.
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/clone="IMAGE:3982036"
/tissue_type="Mammary tumor metastatized to lung. Tu arose spontaneously from a senescent normal mammary clonel outgrowth infected with the virus MMTV."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                Volume MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Sequencing Center
Genter code: BCM-HGSC.
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
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larity 77.0%; Pred. No. 7.2e-198;
Conservative 0; Mismatches 318;
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Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
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/strain="CZECH II"
GI:20072707
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                                                                                                                                                                                       Strausberg, R.
Direct Submission
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3124 bp mRNA linear HTC 20-SEP-2002 Mus musculus, Similar to thymidylate kinase family LPS-inducible member, clone IMAGE:3982036, mRNA.

DEFINITION RESULT 2 BC027329

ACCESSION

HTC 27-MAR-2003

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GAAACATCTACATCCACCATTTGTTATGCAGTGTTCCCAAATTTCTGTTCTACAAGCATG 1485
                      Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3214)
                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (17-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 105 Row: p Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein
This clone has the following problem: frame shifted.
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Contact: MGC help desk
Bmail: cgapbs-remail.nih.gov
Tissue Produrement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Brin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Pred. No. 2.9e-195;
0; Mismatches 318;
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/clone lib="NIH MGC 94"
/lab host="DH10B"
/note="Vector: pCMV-SPORT6"
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6494087"
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Mus musculus
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BC048910.1 GI:29294752
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OY 1309 TIGHTGGGGGCCCTCGAGAGGGGGGGGGGGGGGGGGGGGGGG		REFERENCE 2 AUTHORS Carninci, P., Shibata, Y., Itoh, M., Konno, H., Okazak TITLE Normalization and subtrac prepare full-length cDNA JOURNAL CA0499374 PUBMED 11042159 REFERENCE Shibata, K., Itoh, M., Aiza AUTHORS Konno, H., Akiyama, J., Nis Sumi, N., Ishii, Y., Nakamu Yamamoto, R., Matsumoto, H. Fujiwake, S., Inoue, K., To Yoneda, Y., Ishii, Y., Nakamu Yamamoto, R., Matsumoto, H. Fujiwake, S., Inoue, K., To Yoneda, Y., Ishikawa, T., O Okazaki, Y., Muramatsu, M., TITLE RIKEN integrated sequence sequencing pipeline with JOURNAL Genome Res. 10 (11), 1757 MEDLINE 20530913 REFERENCE 4	AUTHORS THE RIKEN Genome Explorat FANYOW Consortium. TITLE FUNCTIONAL NATURE 409, 685-690 (2001 REFERENCE THE FANTOM CONSORTIUM and Group Phase I & II Team. TITLE Analysis of the mouse tra of 60,770 full-length CON JOURNAL Nature 420, 563-573 (REFERENCE (bases I to 3022) AUTHORS Adachi,7. Alzawa,K., Aka AUTHORS Adachi,7. Alzawa,K., Aka ATAKAWAT., BONO,H., Carl FULUNO,M., HARAGAK,T., IMOO
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GGRGOEKTKEEAELBANNV FRQKVEMTYQRMBNSCHLVDASEBRETVLGKVLELIQS
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                                                                                                                                                                                                                                                                                                                                                        Submitted (10-UUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp, Tel:81-45-503-9222,
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Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
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Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
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/clone_lib="RIKEN full-length enriched mouse
/dev stage="adult"
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Pred. No. 4.4e-195;
0; Mismatches 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="FANTOM_DB:1200004E04"
/db_xref="taxon:10090"
/clone="1200004E04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
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'db_xref="GI:12835871"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="C57BL/6J"
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/note="putative"
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77.1%;
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Homo sapiens (human)
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End constructed (Quoble-strand cDNA was digested with Not I and cloned
into the Not I and EcoRY sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1572.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CSODH005DG06QP1&c=1572.r.
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CELLS (JURKAT CELL LINE) Homo sapiens CDNA
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Li, W. B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
CDNA 13, 2001)
Cn May 13, 2003 this sequence version replaced gi:30647154.
Contact: Genoscope
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/tissue_type="T_CELLE_IUNE"
/cell_line="UURKAT_CELL_LINE"
/cell_line="UURKAT_CELL_LINE"
/note="Vector: pCMVSPORT_6; lst strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned ithe Not I and cloned; library was not normalized."
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Pred. No. 2.8e-171;
0; Mismatches 6; Indels 7;
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/db_xref="taxon:9606"
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full-length cDNA clone CSODHOOSYN12 of T cells (Jurkat cell line) of Homo sapiens (human).
CR623316
CR523316
CR523316.1 GI:50504123
HTC; CNSI.7 ADMY
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1287)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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                                                                                   1749 AGACCCCGGGAGCCTCTGCTTCTCCTACACTGGCATGCTGATGAGATCGTGACATGCCCAC
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                                                                                                                       Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1287;
                                                                                                                                                                                                                                                                                                                                                                           /clone="CSODHOO5XN12"
/tissue type="T cells (Jurkat cell line)"
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 771.4; DB 3;
Pred. No. 2.9e-171;
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                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                   division of Invitrogen.
Location/Qualifiers
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TITLE
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AUTHORS
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JOURNAL
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/docte=="Lataku:joop"
/done="NAGE:30511964"
/tissue_type="Brain glioblastoma"
/lab hose="blu08 (TI phage-resistant)"
/done lib="NH MGC 192"
/done lib="NH MGC 192"
/done lib="NH MGC 192"
/note="Vector: pExpress!; Site_1: Smal; Site_2: Not!; The library was constructed by reverse transcription of 1 ug mRNA using the oligo dT primer GCGCCCC(T) 20 and an RNaseH + MMLV reverse transcriptase. Second strand synthesis was carriaed out by standard methods. The cDNA was size selected by agarcse gel for > 1.2 kb, digested with Not I and directionally cloned into the vector Express-1 at the Smal/Not! sites. DNA from the primary library was used for in vitro transcription from the T7 promoter to produce biotinylated RNA transcripts. These biotinylated transcripts, and wrimer regions were
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                                                            656 GTTTGTTGTTTTTTTTTACACAAACTTAATTTGTCTTTAAATAAGTAC-AGTGGA 714
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 949)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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/mol_type="mRNA"
/db_xref="taxon:9606"
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stranded circles which were repaired by primer extens and transformed back into E. coli resulting in the normalized library. Average insert size 2.0 kb. 3' linker/adator sequence GCGCCCCC(T)20. This libary constructed by Agencourt Bioscience."
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                                                                                                                  Length 949;
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                                                                                                                  Score 741.8; DB 6;
Pred. No. 2.8e-164;
0; Mismatches 13;
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BG501037 757 bp mRNA linear EST 27-MAR-2001 602546443F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4668683 5', mRNA sequence.

LOCUS

RESULT 8 BG501037

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in cloning
                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONFTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCML49p row: f column: 12
High quality sequence stop: 731.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="adenocarcinoma"
/lab host="DH10B (T1 phage-resistant)"
/lab host="NH1MGC_60"
/lone_lib="NIH_MGC_60"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: Sfil (ggcggctcggcc); Site_2: Sfil
/ggcdatatggcc); Double-stranded cDNA was prepared fro
cell line NNA. S. and 3, adaptors were used in clonin
follows: S' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGAGAAAAGGTCCTGCAGACAGTATTAAGCCTAATCCAGAATAGTTTTAGTGAACCGT
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                                                                                                                                    1 (bases 1 to 757)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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5'-ATTCTAGAGGCCGAGGCGGCGACATG-dT(30)BN-3' (where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
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Pred. No. 4.3e-152;
0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4668683"
                   GI:13462554
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                                      EST.
Homo sapiens (human)
                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                   Homo sapiens
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Best Local Similarity
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759 bp mRNA linear EST 27-MAR-2001
60 Homo sapiens cDNA clone IMAGE:4665484 5',
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kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."
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                                                                                                                                                                                                                                                                                       1525 ACTITCAGCCATCGIACCTICITCIGACTGATGGACCCGTCATCACAAAGGICCCTCTCAI
                                                                                                                                                                                                                                                                                                                        1 ACTTCAGCCATCGTACCCTCTTCTGACGATGGACCCGTCATCACAAGGTCCCTCTCAT
                                                                                                                                                                                                                                                                                                                                                                                                      CATGLTCCAGTGAGAGGCCAGCGATTGCTTTCTTCCTGGCATAGTAAACATTTTCTTGGA
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Pred. No. 6.6e-151;
0; Mismatches 11;
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97.9%;
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Homo sapiens
                                                                                                                                                                                                                                  735; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                               AAGACCTGTCTTACTCAGACAGCACCAGGTGTACAGAAGCAGCAGACAAGATCTTCCAGA 1739
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5'-ATTCTAGAGGCGGCGGCGGCGATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.5
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 767)
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/tissue_type="adenocarcinoma"
/lab_host="DH10B (TI phage-resistant)"
/close="DH10B (TI phage-resistant)"
/close="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: Sfil (ggocgoctoggoc); Site 2: Sfil
(ggccattatggc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and in the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the
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NIH-MGC bttp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Conteat: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Gistribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM922 row: i column: 17
High quality sequence stop: 760.
Location/Qualifiers
                                CCGTCATCACAAAGGTCCCTCTCATCATGTTCCAGTGAGAGGCCAGCGATTGCTTTCTTC
                                                                                                                                                    CTGGCATAGTAAACATTTTCTTGGAACATATGTTTCACTTAATCACTAACAATATCTGG
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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3, adaptor sequence: 5.-CACGGCCATTATGGCC-3' and adaptor sequence: 5.-ATTCTAGAGGCGGGGGCCGACATG-dT(30)BN-3' (where B = A, C, or G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo, CA)."
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Site_l: Sfil (ggccgctcggcc); Site_2: Sfil
/ggccattcaggcc); Double-stranded cDNA was prepared from cell line RNA. 'S and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                   AGTAAACATTTTCTTGGAACATATGTTTCACTTAATCACTACCAAATATCTGGAAGACCT
                                                                                                                                                                      481 GICTTACTCAGACAGCACCAGGTGTACAGAAGCAGCAGACAAGATCTTCCAGATCAGCAG
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                                                                                                      GTCTTACTCAGACAGCACCAGGTGTACAGAAGCAGCAGACAAGATCTTCCAGATCAGCAG
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINE)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINE at:
http://image.llni.gov
Plate: LLCM2351 row, o column: 03
High quality sequence stop: 572.
High quality sequence stop: 572.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ATCC
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                     Chordata; Craniata; Vertebrata; Buteleostomi;
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                                                     Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 759)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LINL at:
http://mage.lln.gov column: 05
Plate: LLCM1471 row: a column: 05
High quality sequence stop: 736.
I.ocation/Qualifiers
I. 759
//organism="Mainter"
                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Pred. No. 1.9e-148;
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                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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ilarity 95.8%;
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                              Gaps
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                                                            GTCCTACCAGCGGATGGAGAATCCTGGCTGCCATGTGGT
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Pred. No. 2.5e-143;
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Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 705)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                      GI:14048666
                                                                                                  Homo sapiens (human)
                                                                                                                 Homo sapiens
                                                                      BG778349.1
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LOCUS DEFINITION

BG778349

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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5'-ATTCTAGAGGCGGGGGGGGGATG-dT(30)BN-3' (where B = A, C, G, Or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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II. (bases 1 to 844)

III. (Mac. http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                   657
                         539 TGATCTTGTGTCTGAGGCTCAGAGCCCTTTTGATAGGCTTCTGA-GTCATATATAAAGAC 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tobhyluki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Gnomics, Inc.
Clone distribution: MGC Consortium/Link at:
Phttp://image.llh.gov
Plate: LimMil69p row: e column: 04
High quality sequence stop: 726.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                   598 ATTCAAGCCAAGATGCTCCAACTGCAATATTACCAACTTCTCTGAATTATATTTTGCTT
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1 (bases 1 to 833)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                  2101 ATTIATATTCTTTTTTTTTTTTTTTTAAGAATTGGCTCTGAATAGAATG 2149
                                                                                                                                                                                                                                                                                                                658 ATTTATATTTCCTTTCTAAAGTA-TGGCTCTGAATAGAATG 705
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Pred. No. 9.3e-142;
); Mismatches 24;
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/mol_type="mRNA"

/done="TNAGE:5276907"

/issue_type="hippocampus"

/iab host="Bh108"

/clone_lib="NH4 MGC 95"

/note="Organ: brain; Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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BIS51715.1 GI:15439040
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larity 95.4%;
Conservative
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VERSION
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BISS1715
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96.1%; Pred. No. 5.2e-134;
cive 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .720
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4659044"
                                                                                                                                                               mRNA sequence.
BG496231
BG496231.1 GI:13457747
                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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Matches 693; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1438 ICCACCATITGITATGCAGTGITCCCAAATTTCTGTTCTACAAGCATGTTGTGTGGCAGA 1497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1078 CCAGCACCTGCCCCCAGCCCATCACCCTGTGTACCAGTGGCCAGAGGACCTGCTCAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1138 TGACCTTATCCTGCTGCTCACTGTGAGTCCTGAGGAGGGTTGCAGGGCTGCAGGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGACCTTATCCTGCTGCTGTGAGTCCTGAGGAGGTTGCAGAGGTGCAGGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 GTAGTTACTCTGGCCAGGTGCCACGTCTAACTAGATTAGATGTCGTTTGAAACATCTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1558 ACCCGICATCACAAAGGICCCICTCAATGIICCAGIGAGAGGCCAGCGAIIGCITITCI
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column: 22
                                                                                                                                   /organism="Homo sapiens"
                            High quality sequence stop: 631.
Location/Qualifiers
                                                                                                                                                                                                                                         clone="IMAGE:4806117"
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Best Local Similarity
Matches 626; Conserv
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                                                                                                      source
                                                               FEATURES
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/Lissue type="muccopidermoid carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NH1 MGC 59"
/clone lib="NH1 MGC 59"
/rote="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccatcatggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGCGGACATG-dT(30)BN-3'
(Where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC 1616 EST 27-MAR-2001 9 1617 TTCCTGGCATAGTAACATTTTCTTGGAACATATGTTTCACTTAATCACTACCAAATATC 1676 1677 TGGAAGACCTGTCTTACTCAGACAGCACCAGGTGTACAGAAGCAGCAGAACAAGATCTTCC 1736 1737 AGATCAGCAGGGAGACCCCGGAGCCTCTCCCTACCACTGGCATGCTGATGAGATCG 1796 121 181 241 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 720)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) 61 BG496231 72-MAR-20 bp mRNA linear EST 27-MAR-20 602538182F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4659044 5', þe 2 GACCCGTCATCACAAAGTCCCTCTCATCATGTTCCAGTGAGAGGCCAGCGATTGCTTTC 1557 GACCCGTCATCACAAAGGTCCCTCTCATGTTCCAGTGAGAGGCCAGCGATTGCTTTC 182 AGATCAGCAGGGAGACCCCGGAGCCTCTGCTTCTTACTACACTGCCATGCTGATGAGATCG Trccrggcaratcararcarrrrcrrggaacararargrrrcacrracraccaaararc 122 TGGAAGACCTGTCTTACTCAGACAGCACCAGGTGTACAGAAGAGCAGCAGACAAGATCTTCC Gaps DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lefound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1454 row: d column: 21
High quality sequence start: 6
High quality sequence stop: 696.
High quality sequence stop: 696. Inc. n (LLNL) . 9 Length 720; Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Strausberg

CDNA Library Preparation: CLONETECH Laboratories, Incoma Library Arrayed by: The I.M.A.G.E. Consortium Indels

	1857 ATCTCCCTCAGTCCCAAATTCTAGTAGCCAAGTGTTCCTGCAGAGCTGTCTATGTGTCC 1916	302 ATCTCCCTCAGTCCCCAAATTCTAG-AGCCAAGTGTTCCTGCAGAGGCTGTCTATGTGTCC 360	1917 IGGCIGCCCAAGGGACACICCTGCAGAGCCATITITGGGIAAGGAACACTTACAAAGAAG 1976	361 TGGCTGCCCAA-GGACACTCCTGCAGAGCCATTTTTGGGTAAGGAACACTTACAAGAAG 419	1977 GCATTGATCTTGTGTCTGAGGCTCAGAGCCCTTTTGATAGGCTTCTGATGTCATTAA 2036	420 GCATTGATCTTGTGTCTGAGGCTCAGAGCCCTTTTGATAGGCTTCTGAGTCATATAAC 479	2037 AGACATTCAAGCCCAAGATGCTCCAAATATACCAACCTTCTCTGAATTATATTT 2096	480 AGACATTCAAGCCAAGATGCTCCAACTGCAAATATACCAACCTTCTCTGAATTATA-1TT 538	2097 GCTTATTATATTTCTTTTCTTTTTTCTAAAGAATTGGCTCTGAATAGAATGT 2156	539 GCTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	2157 ICCATCTGAACTGGATGCATATCATTTAGCCAATCCAGTAATTTATATATA	599 TICCAITGAACIGGAIGCAITICAITIAGCCAA-CCAGIAAITIAICIAIAITAATCIAI 657	2217 ACAT-AATATGTTTCCTCAGCATA-GGAGCTATGATTCATTAATTAAAAGTGGAGTCAAA 2274	658 ACATAAATGITICCTCAGCATAGGGAGCTATGATICATTACTTAAACGTGGAGTCAAA 717	2275 A 2275	718 A 718	
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search completed: October 22, 2004, 20:20:39
Job time : 7932 secs

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October 22, 2004, 18:08:37; Search time 1219 Seconds (without alignments) 10806.892 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 1, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 720, App	Sequence 3, Appli	Sequence 3, Appli	Sequence 104, App	Sequence 2642, Ap	Sequence 5564, Ap	Sequence 827, App	Sequence 11496, A	Sequence 7362, Ap
	D	US-10-277-032-1	US-10-681-223-1	US-10-305-810-6	US-10-044-090-720	US-10-277-032-3	US-10-681-223-3	US-10-264-237-104	US-09-867-701-2642	US-09-783-590-5564	US-10-240-425-827	US-09-783-590-11496	
	ngth DB	2571 14	16	15	13	14	16	1579 16	σ	σ	16	σ	
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	Score	2571	2571	2276	2125.2	1130.4	1130.4	1035.4	303.8	219.4	149.8	126.2	79.8
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	13	79.8		9025608	15	US-10-156-761-1	Sequence 1, Appli
	14	92	3.0	1413	10	9-953-3	51,
	15	26		1413	15	10-267-25	51,
	16	26	•	53500	10	09-953-348-	ce 76,
	17	26		ന	15	US-10-267-255-76	e 76,
	18	75.8		667	17	5	463
	19	75		1092		US-10-767-701-9739	9735
U	20	74		1860	15	US-10-156-761-1558	1558
υ	21	74	2.9	9025608	15	10 - 15	9
	22	73		1437	Н	US-10-156-761-5988	5986
	23	71.8		1041	Т		85
U	24	71.6	2.8	2561	σ,	US-09-976-740-48	48,
υ	25	71.6		2561	Н	-10-023-529-4	e 48
U	56	71.6	2.8	2561	Н	4	Sequence 48, Appl
O	27	71.6		2561	Н	9-01-	48
υ	28	71.6	2.8	2561	Н	US-10-671-242-48	9 48
	29	71		1388	Ч	-10-767-701-142	e 14
U	30	7.1	2.8	1734	Н	-10-156-76	e 64'
	31	7.0		15738	٦	0-329-079-4	e 46
	32	7.0	2.7	61944	15	10-329-079-3	34
	33	8		606	11	-09-758-759-	15
	34	68.8	2.7	109519		US-09-758-759-1	Sequence 1, Appli
υ	35	θ,		45		369-49	31
		67.2		1618		US-10-104-047-1463	1463,
	37	9		94	17	US-10-437-963-49955	4995
		66.4		84		437-963-221	221
		9	•	52	10	09-873-367C-1	159
υ	40	99	5.6	924	15	-10-156-761-118	118
	41	99		1521	15	US-10-156-761-3755	375
บ	42	ø		72	17	10-324-96	35,
	43	'n		763	17	10-437-963-49	493.
	44	9:59	2.6	3957	15	US-10-200-562-193	1.93,
	45	ın	2.6	3957	15	US-10-237-551-193	19

ALIGNMENTS

421 CTTCCTGCTGCGGACCCCCTGGATGACCCTGACGCCAAGCGCTGCTCGAGCTGCT 480 421 CTTCCTGCTGCGGACCCCCTGGATGACCCTGACGCCAAGCGCTGCTCGAGCTGCT 480 422 CTTCCTGCTGCGACCCCCTGGATGACCCTGACCCCGGCAAGCGCTGCTCGAGCTGCT 480 431 GGGCGCTGCCAGGAGGACCACGCCCGCACTTGGGCGAGTTCGAGGCCGACCCGCGGGG 540 431 GGGCGCTGCCAGGAGGCACCACGCCCGCACTTGGGCGAGTTCGAGGCCGACCCGGCGG 540 431 GGGCGCTGCGCAGGAGGCACCACGCCACTTGGCGAGTTCGAGGCCGACCCGGCGG 540 541 CCAGCTGTGGCAGCCCTCTGGAGGTGCAAGACGGCAGGCGGTGCGC 600 541 CCAGCTGTGGCAGCCCTCTGGAGGTGCAAGACGGCAGGCGGTGCGC 600 601 ACAGGTCGTGCCGCTCCCGGAGCCCCCGCTGCAGCTGCCAGTTC 660 601 ACAGGTCGTGCCCGCTCCCGGAGCCCCCGGTGCCCCGGTGCCCAGTTC 660	661 CGTTGGTGTTTTCCCGGAACCCGCGGGCCGTTTTTGGAGGACTGTACCTCTTTAT 720 661 CGTTGGTACCCCGGAACCCGCGGGCCGTTTTTGGAGGACTGTACCTCCTTTAT 720 721 TCCTGAACCCCGGGCATGCTTGACCTGGCACAGTGCCCAAAACCAGTCCCCGTAAAGG 780 722 TCCTGAACCCGGGCATGCTTGACCTGGCACAGTGCCCAAAACCAGTCCCAGTAAAG 780 723 TCCTGAACCCGGGCATGCTTGACCTGGACCAGTGCCCAAAACCAGTCCCAGTAAAG 780 724 TCCTGAACCCGGGCATGCTTGACCTGGACCAGTGCCCAAAACCAGTCCCAGTAAAG 780 725 TCCTGAACCAGGCATGCTTGACCTGACCAGTGCCCAAAACCACCCAGTGACCAGAAGG 780 781 AAAGTTCCAGGTTGCATTCACACAGACTGAACCACCACCCTCTTGGCG 780 781 AAAGTTCCAGGTTGCATTCACACAGACTGAACCACCACCCTCTTTGGCG 780 781 AAAGTTCCAGGTTGCATTCACACACACACACACCCACCCTCTTTGGCG 780 781 AAAGTTCCAGGTTGCATTAACACACACACACACCCACCCTCTTTGGCG 780 781 AAAGTTCCAGGTTGCATTAACACACACACACACACCCACC
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QY 2341 CAAGTGGATCTTGGAGATTTCTTGGTAAATTATCTTGCACTTGAATGTCTCATGAT 2400 Db 2341 CAAGTGGATCTTGGAGTGGGATTTCTTGGTAAATTATCTTGCACTTGAATGTCTCATGAT 2400 QY 2401 TACATATGAAATGGTTTGACATATCTTTAGACAGAAAAAAGTGGTGAGGGGAA 2460 Db 2401 TACATATGAAATGGTTTGACATATCTTTAGACAGAAAAAAAGTGGTGAGGGGAA 2460 QY 2461 ATTATAGAAGTTGTGAATTTAGAGAAAAAAAAAAAAAA	PRESENT 2 - 23 - 1 UNE-10.681-22-1 DE-20.681-22-1 DE-20.681-22-1 DEPARTICANT: MIDSOMANORS1998A1 APPLICANT: MIDSOMANORS1998A1 APPLICANT: MIDSOMANORS1998A1 TITLE OF INVENTION: AND WELCULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: ALLD MULECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: ALLD MULECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: ALLD MULECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: ALLD MULECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: ALLD MULECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: ALLD MULECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: ALLD MULECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: ALLD MULECULES ENCODING HUMAN KINASE PROTEINS, AND USES PRIOR APPLICATION NUMBER: 10/10-09 PRIOR PRINCE ALLD MULECULES ENCODING HUMAN KINASE PROTEINS, AND USES PRIOR APPLICATION NUMBER: 10/10-09 PRIOR AP

5-810-6 and by Application US/ arion No. US200301763 L INFORMATION: CANT: UJ, Jingfang CANT: Thang, Haihong CANT: Simons, Jan Fx CANT: Tailon, Bruce CANT: Tailon, John Fx CANT: Smichs, John Fx CANT: Smithson, Glen CANT: Smithson, Glen CANT: Millet, Isabel OF INVENTION ANTISE NT APPLICATION NUMBER: FILLING DATE: 2001-12 APPLICATION NUMBER: FILLING DATE: 2001-11 APPLICATION NUMBER: FILLING DATE: 2001-11 APPLICATION NUMBER: FILLING DATE: 2001-12 APPLICATION NUMBER: FILLING DATE: 2001-12 APPLICATION NUMBER: FILLING DATE: 2001-12 APPLICATION NUMBER: FILLING DATE: 2001-12	PRIOR APPLICATION NUMBER: 60/192,838 PRIOR FILING DATE: 2000-03-29 PRIOR FILING DATE: 2000-04-03 PRIOR PILING DATE: 2000-04-03 PRIOR PILING DATE: 2001-09-19 PRIOR PILING DATE: 2001-09-19 PRIOR PILING DATE: 2001-09-19 PRIOR PILING DATE: 2001-09-19 PRIOR PILING DATE: 2000-09-19 PRIOR PILING DATE: 2001-10-04 PRIOR PILING DATE: 2000-09-19 PRIOR PILING DATE: 2000-0-11 PRIOR APPLICATION NUMBER: 60/182,637 PRIOR PILING DATE: 2000-02-16 PRIOR PILING DATE: 2000-10-13 Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 47 SEQ ID NO 6 LENGTH: 2856 LENGTH: 2856 TYPE: DNA ORGANISM: Thymidine Kinase	US-10-305-810-6
	1861 CCCTCAGTCCCAAATTCTAGTAGCCAAGTGTTCCTGCAGAGGCTGTCTATGTGTCCTGGC 1920 1861 CCCTCAGTCCCAAATTCTAGTAGCCAAGTGTTCCTGCAGAGGCTGTTTTGTTGTTGTTGTTCTTGTTGTTGTTTTGTTGT	

Qy 1520 AITTTACTTCAGCCATGGTACCTCTTCTGACTGATGGACCCGTCATCACAAAGGTCCCT	QY 1580 CTCATCATGTTCCAGTGAGAGCCAGCGATTGCTTTCTTCCTGGCATAGTAAACATTTTCTCTGTGCTAGTAAACATTTTCTTCTTCTTGCTTTCTTCTTGCTTTTTCTTCTTGCTTTTCTTC	OY 1640 IIGGAACATAIGTITCACITAAICACDACCAAIAICIGGAAGACCIGICITACICAGAC	OY 1700 AGCACCAGGTGTACAGAAGCAGCACACAAGATCTTCCAGATCAGCAGGGAGACCCCGGAG 1615 AGCACCAGGTGTACAGAAGCAGCAGAAGATCTTCCAGATCAGATCAGGAGACCCCGGAG	Dy 1760 CCTCTGCTTCTCCTACACTGCTGATCACTGACATCCTGACATGCCCCACATTGGCTTCTT Db 1675 CCTCTGCTTCTCCTACACTGGCATGCTGACATCGTGACATGCCCACATTGGCTTCTT	AY 1820 CCACATCTGGTTGCACTCGTCATGATGGGCTCGCTTGCATCTCCCTCAGTCCCCAAATTCTA	Ay 1880 GTAGCCAAGTGTTCCTGCAGAGGCTGTCTATGTGTCCTGGCTGCCCAAGGACACTCCTG	Oy 1940 CACAGCCATTTTGGGTAAGGAACACTTACAAAGAAGGCATTGATCTTGTGTCTCGAGGCT	2000 CAGAGCCCTTTGATAGGCTTCTGATGTCATAAGACATTCAAGCCAAGATGCTCC	Qy 2060 AACTGCAATATACCAACCTTCTCTGAATTATATTTTGCTTATTTAT	QY 2120 TTTCTAAAGAATTGGCTCTGAATAGAATGCACATTTTCCATCTGAACTGCATATC	QY 2180 AITTAGCCAATCCAGTAATTTATTTATATATCTATACATAATATGTTTCCTCAGCATA [Qy 2240 GGAGCTATGATTAAAAGTGGAGTCAAAAGCGTAAATGCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	Qy 2300 AFTTCAFTACACAAACFTAATTGTCTTGTAAATAAGTTCAAGTGGATCTTGGAGGG 23	Oy 2360 GATTCTTGGTAAATTATCTTGCACTTGAATGTCTCATGATTACATAGAAATGCTTTG	Oy 2420 ACATATCTTAGACAGAAAAAGTAGCTGAGGGGGGAAATTATAGAGCTTGTGAGA 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Oy 2480 TTTAGGGAGTAGCT 2493	RESULT 4 US-10-044-090-720 ; Sequence 720, Application US/10044090
443 GATGACCCTGACCCGGCGGCGGCGCACAGCAAGGCTTCCTGCTGCGCGCGC	03 CGCCCGCACTTGGGCGAGTTCGAGCCGACCCGCGCGCCGGCTGTGGCAGCCCTCTGG 56 1	GAGGTGCAAAGACGCGGGGGTGCGGGGGGCGCGCGCGCGC	CCCCGGTGCACCGGTGCTGCCAGATTCGTGGTCTTCCGGGAA 68 CCCCCGGTGCACTTGCCCAGTTTCGTGGTCTTTCCGGGGAA 68 CCCCCGGTGCACTTGCCAGATTTCGTGGAA 68 CCCCCGGTGCACTTGCCAGATTTCCTTGGAA	GCCGCCCGGGCCGTTTTGCAGGAGTGTACTCTTTATTCCTGAAGCCCGGGCAGTGCTT	CGACCAGTGCCCAAAACAGATCCAGAAAGTTCCAGGTTGCCATC 80	SGACTGGATGCCACGGGTAAAACCACGGGGACCCAGTCAGTGGCAGATTCACTT 85	AAGGCTGTCCTCTTAAAGTCACCACCTCTTGCATTGGCCAGTGGAGGAAGATCTTTGAT 91	GAIGAACCAACTATCATTAGAACAGCTTTTTACTCTTTGGGCAATTATATGTGGCCTCC 97	GAAATAGCTAAAGAATCTGCCAAATCTCCTGTGATTGTAGACAGCTACTGGCACAGCACG	GCCACCTATGCCATAGCCACTGAGGTGAGTGGGGGTCTCCAGCACTGCCCCAGACTAGCCATAGCCATAGCCATAGCCATAGCCATAGCCACTGAGGTGAGTGA	CACCTGTGTACCAGTGGCCAGAGGACCTGCTCAAACCTGACCTTATCCTGCTCACT 115	CCTGAGGAGAGGTTGCAGAGGCTGCAGGGCCTGGGGCATGGAGAGACCAGGGAA 	1220 GAAGCAGAACTIGAGGCCAACAGIGIGITICGICAAAAGGIAGAAAIGICCIACCAGGGG 1279 	AIGGAGAAICCIGGCIGCCAIGIGGTIGAIGCCAGCCCTCCAGAGAAAAGGICCIGCAG 13 AIGGAGAAICCIGGCIGCCAIGIGGTIGIAIGIGIGIGIGIGIGIGIGIGIGIGIGIGAGAAAGGICCIGCAGAGAAAAGGICCIGCAGAGAAAAGGICCIGCAGAGAAAAGGICCIGCAGAGAAAAGGICCIGCAGAGAAAAGGICCIGCAGAGAAAAAAAA	TGCC 13	ACGICTAACTAGATTAGATGTTGTTTGAAACATCTACATCCACCATTTGTTATGCAGTGT 1	1460 TCCCAAATTCTGTTCTACAAGCATGTTGTGTGGCAGAAAACTGGAGACCAGGCATCTTA 1519

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; Publication No. US20020137081A1
; GENERAL INFORMATION:
APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VAS:
; FILE REFERENCE: PA-0028 US
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL PROGram
; SEQ ID NO 720
; LENGTH: 2645
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                                                                                                                                                                               ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID US-10-044-090-720
                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
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Db 17964 ATGTTGTGGAGAAAACTGGAGCATCTTAATTTTACTTCAGCCATCGTACCC 18023 1543 TC-TTCTGACTGATGGACCCGTCATCACAAGGTCCCTCTCATCATGTTCCAGTGAGAGG 1601 18024 TCTTTCTGACTGATGGACCCGTCATCACAAAGGTCCCTCTCATCATGTTCCAGTGAGAGG 18083 1602 CCAGCGATTGCTTTCTTCTCTGCAAAGGTCCCTCTCATCATGTTCCAGTGAGAGG 18083 1602 CCAGCGATTGCTTTCTTCTCGGCATAGTAAACATTTTCTTGGAACATATGTTTCACTTAA 18143 Qy 1602 CCAGCGATTGCTTTCTTCTGGAAGACCTGTTTCTTGGAACATATGTTTCACTTAA 18143 1722 CAGCGATTGCTTTCTTCGGAAGACCTGTTTTCTTGGAACATATGTTTCACTTAA 18143 Db 18144 CACTACCAAATATCTGGAAGACCTGTTTACTCAGACACACAGGAGGG 18203 Qy 1722 CAGCAAATATCTGGAAGACCTGTTTTTCTTGGACACACAGGAGGG 18203 Qy 1782 ATGCTGATGGAACATGCGAGGAGCCCCGGAGCCTTCTCTCCTACACTGGC 1781 Db 18264 ATGCTGATGGAACATGCCCAATTGGCTTCTTCCACATCTGGTTACTGGT 1811 Db 18264 ATGCTGATGAATCGTGACATGCCCAATTGGCTTCTTCCACATCTGGTTCTCTCTC	18383 GCTGTCTACAAGACTCCGCCAA-GGACTCCTGCAGACCCATTTTTGGTAAGGA 1962 ACACTTACAAGAAGGCATTGATCTTGTGTCTGGGCTCAGAGCCCTTTTTTTT	OY 2262 AGGINGSAGINGAAAACCIAAATGATTGTTGTTGTTGTTGTTAAT 2321 Db 18739 AAGTGGAGTCAAAACGCTAAATGCATGTTTGTTGTTGTTGTTAATTGTTAAT 2321 OY 2322 TTGTCTTGTTAAATAAGTTCAAGTGGATTTCTTGGTAATTTCTTG 2381 Db 18799 TTGTCTTGTTAAATAAGTAC-AGTGGATCTTGGAGTGGGATTTCTTGGTAAATTATCTTG 18857 OY 2382 CACTTGAATGTCAATAAGTAC-AGTGGATCTTGGAGTGGGATTTCTTGGTAAATTATCTTG 18857 OY 2442 GTAGCTGAGTTACATATGAAATCGCTTTGACATAATTTAAGAAAAAA 18917 OY 2442 GTAGCTGAGGGGAAATTATAAGAGTTGTGTGATATTTAAGAGAAAAAA
2132 TTGGCTCTGAATAGAATGCACATTTTCCATCTGAACTGGATGCATATTAGCCAATC 2191 1858 -TGGCTCTGAATAGAATGCACATTTTCCATCTGATTTAGCCAATC 2191 1858 -TGGCTCTGAATAGAATGCACATTTTCCATCATTTTAGCCAATC 2915 2192 CAGTAATTTAATTAATATTATTATATTAATTAATTAATTCCTCAGCATAGGACTATGATT 2251 1916 CAGTAATTTAATTAAATGCTAAATACATAATTCCTCCAGCATAGGACTATGATT 1975 2252 CATTAATTAAAAGTGGAGTCAAAATGCAATGTTTGTTGTGTGTATTTTCATTACA 2311 1976 CATTAATTAAAAGTGGAGTCAAAAAGCTAAATGCAATGTTTGTT	Sequence 3, Application US/10277032 Sequence 3, Application US/10277032 Sequence 3, Application US/10277032 Sequence 3, Application US/10277032 Sequence 3, Application US/10277032 SEQUENCE INFORMATION: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, TITLE OF INVENTION: THEREOF FILE OF INVENTION: OF SEQUENCE TO SE	Duery Match 44.0%; Score 1130.4; DB 14; Length 20966; Best Local Similarity 98.1%; Pred. No. 1.5e-268; Matches 1228; Conservative 0; Mismatches 16; Indels 8; Gaps 8; 1243

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CACTTGAAIGICTCAIGATTACATAIGAAAICGCTTIGACAIATCTTTAGACAGAAAAA 18917
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APPLICANT: Birss et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PAI3191

CURRENT APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR APPLICATION NUMBER: US 60/205,515

PRIOR FILING DATE: 2000-65-19

PRIOR FILING DATE: 2000-65-19

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: Patentin Ver. 3.1

SEQ ID NO 104

LENGTH: 1579
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Best Local Similarity 98.8
Matches 1127; Conservative
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND
TITLE OF INVENTION: THEREOF;
FILER REPERENCE: CLOO1305 D1V-11
CURRENT APPLICATION NUMBER: US/10/681,223
CURRENT APPLICATION NUMBER: US/27/032
PRIOR FILING DATE: 2003-10-09;
PRIOR PELING DATE: 2002-10-22
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSRQ for Windows Version 4.0
LENGTH: 20966
                        AND
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ORGANISM: Homo sapiens
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Matches 1228; Conserv
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Gaps 2;

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Score 303.8; DB 9; Pred. No. 1.1e-64; 0; Mismatches 7;

Length 507;

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121 ACGCTAAATGCAATGTTGTTGTGTATTTTCATTACACAAACTTAATTTGTCTTGTTAAA 180
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                 APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 2642
LENGTH: 507
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                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 97.3%;
Matches 330; Conservative
      APPLICANT: Aglate, Paul A.
                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapien
US-09-867-701-2642
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                                                    AGTGAGAGGCCAGCGATTGCTTCTTCTTGGCATAGTAAACATTTTCTTGGAACATATGT
                                                                                                                    TICACITAAICACIACCAAAIAICIGGAAGACCIGICTIACICAGACAGCACCAGGIGIA
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseline, William A.
APPLICANT: Haseline, William A.
APPLICANT: Li, Haddong
APPLICANT: Roben, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.201
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 200-02-15
PRIOR FILING DATE: 1995-04-12
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR PLING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PAECHLIN Ver. 2.0
SOFTWARE: PAECHLIN Ver. 2.0
300 GGGGAAATTATAGAGC-TGTGTGACTTTAGGGAGTAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or
                                                                                                                                                  Sequence 5564, Application US/09783590 Patent No. US20020110850A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (253)
OTHER INFORMATION: n equals a,t,g,''
                                                                                                                       US-09-783-590-5564
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RESULT 8
8.09-867-701-2642
7.5-09-867-701
7.5-09-867701
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LOCATION: (386) ΟĽ or or Ö or or or NAME/KEY: misc feature LOCATION: (261) OTHER INFORMATION: n equals a,t,g, or LOCATION: (310) OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (315) OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (316) OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature or OT or OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature or LOCATION: (405)
OTHER INPORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (412)
OTHER INFORMATION: n equals a,t,g, ox
NAME/KEY: misc feature
LOCATION: (413) OTHER INFORMATION: n equals a,t,g, LOCATION: (423) OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature LOCATION: (448) LOCATION: (437) OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature LOCATION: (358) LOCATION: (358) OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc_feature OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature LOCATION: (376) LOCATION: (386) OTHER INFORMATION: n equals a,t,g, LOCATION: (394)
OTHER INFORMATION: n equals a,t,g,
NOME/KEY: misc feature
LOCATION: (41)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature LOCATION: (402) OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature LOCATION: (416) OTHER INFORMATION: n equals a,t,g, LOCATION: (432) OTHER INFORMATION: n equals a,t,g, INFORMATION: n equals a,t,g, NAME/KEY: misc feature LOCATION: (381) NAME/KEY: misc feature NAME/KEY: misc feature NAME/KEY: misc feature NAME/KEY: misc feature LOCATION: (301) LOCATION: (366) COCATION: LOCATION: OTHER

1032 ACAGCACCAACCTATGCCATAGCCACTG-AGGTGAGTGGGGGGTCTCCAGCACCTGCCC 1090 972 TGGCCTCCGGAAATAGCTAAAGAATCTGCCAAATCTCCTGTGATTGTAGACAGGTACTGGC 1031 182 ACAGCACCACTATGCCATAGCCACTGAAGGTGAGTGAGGGGGGTCTCCAGCACCACCACCC 241 852 ATTCACTTAAGGCTGTCCTCTTAAAGTCACCCTCTTGCATTGGCCAGTGGAAGA 912 TCTTTGATGATGAACCAACTATCATTAGAAGAGCTTTTTACTCTTTGGGCAATTATATTG 62 ICITIAATGAIGAACCAACIAICATIAGAAGAGCITTIAACICITIGGGCAAITATATIG 122 IGGCCTCCGAAATAGCTAAAGAATCTGCCAAATCTCTGTGAATTGTAGACAGGTACTGC 2 ATTCCCTTAAGGCTGTCCTCTTAAGTCACCACCTCTTGCATTGGCCAGTGGAGGAAGA Gaps Length 497; 8.5%; Score 219.4; DB 9; Length llarity 90.7%; Pred. No. 9e-44; Conservative 0; Mismatches 23; Indels 1091 CCAGCCCATCACCCTGTGTA--CCAGTGGCCAGAGGACCTG 1129 242 CCAGCCCATCANCCTGTGTNACCAGTGGGCCAGAGGACCTG 282 O O υ U O O υ υ υ Sequence 827, Application US/10240425
Publication No. US20040033502A1
GENERAL INFORMATION:
APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe ; LOCATION: (493) ; OTHER INFORMATION: n equals a,t,g, or US-09-783-590-5564 OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (485) OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature or οĭ OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (481) or or oror or or NAME/KEY: misc feature LOCATION: (488) OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature LOCATION: (492) OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (460)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature LOCATION: (470) OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature LOCATION: (487) OTHER INFORMATION: n equals a,t,g, LOCATION: (470)

NOTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (479) a,t,g, OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (467) Query Match Best Local Similarity Matches 255; Conserv RESULT 10 US-10-240-425-827/c LOCATION: g d ò g ò g ð à

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Best Local Similarity
Matches 182; Conserv
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APPLICANT: Haseltine, William A.

APPLICANT: Haseltine, William A.

APPLICANT: Haseltine, William A.

APPLICANT: Haseltine, William A.

APPLICANT: Rosen, Craig A.

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2

FILE REPERENCE: PO-16.2C1

CURRENT APPLICATION NUMBER: U8/09/783,590

CURRENT FILING DATE: 1995-04-12

PRIOR APPLICATION NUMBER: 08/346,731

PRIOR APPLICATION NUMBER: 08/346,731

PRIOR PILING DATE: 1994-11-21

NUMBER OF SEQ ID NOS: 1246-5

SOFTWARE: Patentin Ver. 2.0

LENGTH: 390

LENGTH: 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTGCACTTGAATGTCTCATGATTACATATGAAATCGCTTTGACATATCTTTAGACAGA 2436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       603 TTAATTTGTCTTGTTAATAAGTAC-AGTGGATCTTGGAGTGGGATTTCTTGGTAATTA 545
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APPLICANT: Vockley, Joseph G.

TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue FILE REPERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-09-30
PRIOR PILIATION NUMBER: US/10/240,446
PRIOR PILIATION NUMBER: US 60/193,446
PRIOR PILIATION NUMBER: US 60/193,446
PRIOR PLILIATION NUMBER: US 60/193,446
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 827
                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Genbank Accession No. US20040033502A1 AI742057
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 603;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 149.8; DB 16; Length
Pred. No. 1.7e-26;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (60)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
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Matches 173; Conservative
                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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US-09-783-590-11496
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1563 TCATCACAAAGGICCCTCTCATCATGTTCCAGTGAGGGCCAGCGATTGCTTTCTTCCTG 1622
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ilarity 80.5%; Pred. No. 9.6e-21;
Conservative 0; Mismatches 38;
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UIN
APPLICANT: SHIRBA, TADAYOSHI
APPLICANT: SHIRBA, TADAYOSHI
APPLICANT: SHIRBA, TADAYOSHI
APPLICANT: HATTORI MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: US 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PLING DATE: 2001-05-30
PRIOR PLING DATE: 2001-06-02
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Sequence 1, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:

RESULT 13 US-10-156-761-1

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Pred. No. 5.6e-07;
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
PILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PLING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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FILING DATE: 1996-08-19

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Search completed: October 23, 2004, 01:04:43
Job time : 7138 secs
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Pred. No. 5.1e-08;
0; Mismatches 175; Indels
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APPLICANT: H. Min.
APPLICANT: B. Min.
APPLICANT: B. Min.
APPLICANT: B. Min.
AITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER.
FILE REPERENCE: 600.530US1
CURRENT APPLICATION NUMBER: US/09/953,348
CURRENT APPLICATION NUMBER: PCT/US00/06394
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 153
SOFTWARE PASTSEQ for Windows Version 4.0
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Publication No. US20030124689A1
GENERAL INFORMATION:
APPLICANT: Sheaman, D
APPLICANT: Waco, Y
APPLICANT: Varoglu, M
APPLICANT: Holdon, P
TITLE OF INVENTION: Mitomycin biosynthetic gene cluster:
FILE REFERENCE: 600, 456G91;
CURRENT APPLICATION NUMBER: US/10/267,255
CURRENT FILING DATE: 2002-10-09
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PRIOR APPLICATION NUMBER: US 09/266,965
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: US 08/624,447
                                          ; Sequence 51, Application US/09953348; Publication No. US20030134398A1; GENERAL INFORMATION:
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Best Local Similarity 50.8%;
Matches 181; Conservative
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Varoglu, Mustafa
He, Min
Sheldon, Paul
                                                                                                                                                                            APPLICANT: Sherman, David. H
APPLICANT: Mao, Yingqing
APPLICANT: Varoglu, Mustafa
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LENGTH: 1413
US-09-953-348-51
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US-10-267-255-51
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Pred. No. 5.1e-08;
0; Mismatches 175; Indels
PRIOR APPLICATION NUMBER: PCT/US94/11279
PRIOR FILING DATE: 1994-10-06
PRIOR FILING DATE: 1993-10-07
NUMBER OF SEQ ID NOS: 145
SOFTWARE: PastSEQ for Windows Version 3.0
EED ID NO 51
LENGTH: 1413
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; ORGANISM: Streptomyces lavendulae
US-10-267-255-51
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Best Local Similarity 50.8%;
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Sequence 1, Appli
Sequence 3, Appli
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Query Match Best Local Similarity 100. Matches 2571; Conservative

TYPE: DNA CRGANISM: HomoSapien US-09-984-880-1 LENGTH: 2571

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	APPLICANT: Ming-Hui	ing-Hui	-			
		ENTION:	H	ED	ISOLATED HUMAN KINASE PROTEINS, NUCLEIC	
		OF INVENTION:		MOL	ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,	INASE PROTEINS, AND USES
; TII	TITLE OF INV	ENTION:	THEREOF	OF		
	FILE REFERENCE: CL001305	CE: CLO	101305			
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                                                       Sequence 1, Application US/10277032
Patent No. 6664087
GENERAL INCORMATION
GENERAL INCORMATION
TITLE OF INVENTION: ACID MULECULES ENCORNOR HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCORNOR HUMAN KINASE PROTEINS, AND UTITLE OF INVENTION: THEREOF ELEGIBLE SEPERENCE: CLOO1305 DIV
CURRENT FAPILICATION NUMBER: US/10/277,032
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: 09/984,880
PRIOR PILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%;

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Pred. No. 9.3e-260;
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APPLICANT: Mao, Y
APPLICANT: Mao, Y
APPLICANT: He, M
APPLICANT: Sheldon, P
ATTLE OF INVENTON: Mitomycin biosynthetic gene cluster
FILE REPERENCE: 600.456US1
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CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: US 08/624,447
EARLIER FILING DATE: 1996-08-19
EARLIER APPLICATION NUMBER: PCT/US94/11279
EARLIER FILING DATE: 1994-10-06
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Patent No. 6495348
GENERAL INFORMATION:
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1305 DIV
CURRENT APPLICATION NUMBER: US/10/277,032
CURRENT APPLICATION NUMBER: 09/984,880
PRIOR FILING DATE: 2002-10-31
PRIOR FILING DATE: 2001-10-31
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llarity 98.1%; Pred. No. 9.3e-260;
Conservative 0; Mismatches 16;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 20966
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/10277032 Patent No. 6664087 GENERAL INFORMATION:
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APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
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Pred. No. 1.6e-07;
0; Mismatches 175; Indels
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PUBLICANT: He, M
PUBLICANT: Sheldon, P
TITLE OF INVENTION: MICOMYCIN DIOSYNTHELIC Gene cluster
FILE REFERENCE: 600.45603.
CURRENT APPLICATION NUMBER: US/09/266,965
CURRENT FILING DATE: 1999-03-12
FEARLIER FILING DATE: 1996-08-19
FEARLIER FILING DATE: 1994-10-06
EARLIER FILING DATE: 1994-10-06
EARLIER FILING DATE: 1994-10-06
EARLIER FILING DATE: 1994-10-06
SEARLIER FILING DATE: 1993-10-07
FEARLIER FILING DATE: 1993-10-07
SOFTWARE: FASTSEQ for Windows Version 3.0
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                         EARLIER APPLICATION NUMBER: US 08/133,963
EARLIER FILING DATE: 1993-10-07
NUMBER OF SEQ ID NOS: 145
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 51
LENGTH: 1413
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US-09-266-965-51
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APPLICANT: ALM, SAIMON W.

ITILE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-07-14
PRIOR PLING DATE: 1997-10-26
PRIOR PLING DATE: 1997-10-26
PRIOR PELING DATE: 1997-10-26
PRIOR PELING DATE: 1997-06-03
PRIOR PELING DATE: 1997-06-03
NUMBER OF SEQ ID NOSES 53
SOFTWARE: FREUESC for Windows Version 4.0
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49.1%; Pred. No. 3.7e-07;
tive 0; Mismatches 279;
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Pred. No. 8.5e-05;
0; Mismatches 292;
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION UNMERR: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VEY: 2.1
SSOFTWARE: PATENTIN VEY: 2.1
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ORGANISM: Mycobacterium tuberculosis
FEATURE:
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Pred. No. 3.5e-05;
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Patent No. 6294328
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, John TITLE OF INVENTION: TURBRCULOSIS
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN J.
TITLE OF INVENTION: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NOS: 2
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CTHER INFORMATION: H37RV
US-09-103-840A-1
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Patent No. 5773249
GENERAL INFORMATION:
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Frotein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: 4 EMBACCAGERO Center, Suite 3400
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REGISTRATION VUNDRER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
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SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US
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CLASSIFICATION: 435
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APPLICATION NUMBER: US/08/642,255
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Pred. No. 1.3e-06;
0; Mismatches 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: High Molecular Weight Col
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8701
TELEFAX: (415) 494-8771
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Patent No. 5773249
GENERAL INFORMATION:
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TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 60
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ATTORNEY/AGENT INFORMATION:
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; ORGANISM: Epstein-Barr virus
US-09-410-399-3
                            ; SEQ ID NO 2
LENGTH: 1926
; TYPE: DNA
; ORGANISM: Epstein Barr Vi
; FEATURE:
; NAME/KEY: CDS
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     SOFTWARE: Patentin
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US-09-249-585A-2/c
Sequence 2, Application US/09249585A;
Patent No. 6417002
GENERAL INFORMATION:
TATLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
TILE REFERENCE: 0867/00905
CURRENT APPLICATION NUMBER: US/09/249,585A;
UNMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                          Length 756;
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Pred. No. 2.4e-06;
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                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic"
TELEPHONE: (415) 494-8700
TELERAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                          2.6%;
                                                                                                                                  LENGTH: 756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                             287; Conservative
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Best Local Similarity
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Parent No. 6482587

Parent No. 6482587

Parent No. 6482587

Parent No. 6482587

APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.

TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral ITLE OF INVENTION: to Genomic Host DNA

FILE REPERRICE: UM-03778

CURRENT APPLICATION NUMBER: US/09/410,399

CURRENT FILING DATE: 1999-10-01

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO.3
                                                                                                                                                                                                                                   GOGCCCATGGCCTTCGCCCCGCCGGCTCCTGCGCGGCCACTGTCGGGGCCGCTCTTCGG
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                                                                                            / Match 2.5%; Score 64; DB 4; Le:
Local Similarity 46.3%; Pred. No. 2.1e-05;
les 211; Conservative 0; Mismatches 245;
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; LOCATION: (1)..(1926)
; OTHER INFORMATION: coding strand of EBNA-1 DNA US-09-249-585A-2
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REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
                                                                                                                Mismatches
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APPLICATION NUMBER: US/09/359,08:
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NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Hiang, Betty
Payan, Don
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CORRESPONDENCE ADDRESS:
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                                                                                                                    Matches 211; Conservative
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ZIP: 94111-4187
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                                                                                  Best Local Similarity
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US-09-050-863-2
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Patent No. 611411
GENERAL INFORMATION:
APPLICANT: Lao, Ying
APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
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4 Embarcadero Center, Suite 3400
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COMPUTER READBALD FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve:
CURRENT APPLICATION DATA:
APLICATION NOMBER: US/09/050,863
FILING DATE: 30-MR-1998
CLASSIFICATION:
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NAME: S11va, RODIN M.
FEGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A--
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TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 2580 base pairs
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EDNESS: unknown
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STREET: 4 Embarcaderc
CITY: San Francisco
STATE: CA
COUNTRY: USA
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STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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TELECOMMUNICATION INFORMATION:
TELEPAR. (415) 781-1989
TELEFAR. (415) 949-8711
JINFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
MOLECULE TYPE: UNKNOWN
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-359-081-2
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Job time : 235 secs
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Ada38100 Thymidine
Adc39115 Novel hum
Adh4258 Novel hum
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Adm10601 Human thy
Abx63720 Human cDN
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Adh42564 Novel hum
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ALIGNMENTS

Beasley EM, Difrancesco V; Human cDNA encoding a novel kinase protein. Human; ss; gene; kinase; chromosome Location/Qualifiers 32. .1381 /*tag= a /product= "Kinase" ADC63369 standard; cDNA; 2571 BP. 22-OCT-2002; 2002US-00277032. 31-OCT-2001; 2001US-00984880. (first entry) (APPL-) APPLERA CORP Ketchum KA, US2003087294-A1 sapiens 18-DEC-2003 08-MAY-2003

WPI; 2003-765435/72. P-PSDB; ADC63370.

Novel isolated human kinase protein useful for drug screening assays, as a target for diagnosing disease, pharmacogenomic analysis, and for identifying compounds that modulate kinase activity.

Claim 22; SEQ ID NO 1; 48pp; English

The invention relates to an isolated peptide consisting of or comprising an amino acid sequence chosen from an amino acid sequence of human kinase protein (ADC63370), an allelic variant of the kinase, orthologue or fragment. Also included are an isolated antibody that selectively binds

indicate that normalize the first seek protective that competitive indicates that increase with kinase, pharmacogenomic analysis and treating a disorder characterised by an absence of inappropriate or unwanted expression of the protein, useful as target spot diagnosing active protein activity, disease or predisposition to disease. The nucleic acid is useful for assessing expression in disease states, diagnostic tools as an immunological marker for aberrant protein for inhibiting protein function, tissue typing. The nucleic acids are useful for facilitating protein trafficking or facilitate manipulation of a protein for assay or production, probes, primers, chemical intermediates, constructing recombinant vectors, expressing antiquency portions of the proteins, for determining chromosomal positions of the nucleic acid molecules, for making vectors containing the gene regulatory regions, as hybridisation probes for determining the presence, level, form and distribution of nucleic acid expression. The gene encoding the kinase is located on human chromosome 2. The present comprising the nucleic acids, a host cell containing the vector, detecting the presence of the kinase in a sample, detecting the presence of the mucleic acids in a sample, a pharmaceutical composition comprising a kinase binding agent, treating a disease or condition mediated by a human kinase protein and identifying a modulator of the expression of the kinase involves. The kinase is useful for identifying a modulator, for identifying an agent that binds to the kinase, for biological assays related to kinases, drug screening assays, identifying compounds that modulate kinase activity, to screen a compound for the ability to stimulate or inhibit interaction between the kinase protein and a stimulate or inhibit interaction between the kinase protein and a proteins detailed above (appearing as the cDNA, ADC63369, and gene, ADC63371), a gene chip comprising the nucleic acids, a transgenic non-human animal comprising the nucleic acids; a nucleic acid vector for competitive kinase, an isolated nucleic acid molecule encoding the kinase molecule that normally interacts with kinase protein,

Sequence 2571 BP; 561 A; 711 C; 675 G; 624 T; 0 U; 0 Other;

ö 120 180 240 CGCCCCGGGCGACGCAGACGCCCCCGACCCCGCCTTGGCGGCGCTGTTGGGGGCCCCCGGGA 240 120 180 300 420 420 480 480 540 GGCGGCGCGCGCGCACCAGCTGCTGCACCAGCTGCGCCGCGCCCCTTCCAGCGGTG 360 edececcreccaedacacacaceccecacriredeceacrireaeceaacreaacceaacceee 540 09 9 CCAGCTGCTCAGGCTGCTCTGCTACTGCCCGGGCGGCCAGGCCGGCGGCGCCACAGCAAGG 1 casaccasasascarcarrasascarcarrasacrarasacrarasacrarasacrarasasas GCGCAGCTACTCGCTGTGCGTGCCCGTGACCCCGGACGCCGGGCTGCGGGGCCCGGGTCCG GCCACTGTCGGGGCCGCTGCTCGGGCGCCGCGCGGGTCTGCGCTTGGGGGCCATGGCTCCGCC 61 GCCACTGTCGGGGCGCTGCTCGGGCGGCGGGGTCTGCGCTGGGGGCCATGGCTCCGCC GTGCCGCTTCGTCCTGGAGCTTCCCGACTGCACCCTGGCTCACTTCGCCCTAGGCGCCCGA GGGCGCCTGCCAGGAGGCACCACGCCCACTTGGGCGAGTTCGAGGCCGACCCGCGCGG CGCCCCCGGCGACGCACACGCCCCCGACCCCCGCCTGGCCGCCTGTTGGGGCCCCCGGA CTTCCTGCTGCGCGACCCCTGGATGACCCTGACACCCGGGAAGCGCTGCTCGAGCTGCT criticardedecarecerearidaecericaedecadecadedecreereereer Gaps DB 10; Length 2571; 0; Indels 0 100.0%; Score 2571; 100.0%; Pred. No. 0; iive 0; Mismatches Query Match
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δÿ	1141	CTGCTGCTCACTGTGAGTCCTGAGGAGAGGTTGCAGAGGCTGCAGGGCCGGGG 120
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Db	1441	CCATITETTATECAGTETTCCCAAATTCTGTTCTACAAGCATGTTGTGTGTGTGTAAAAA 15
δý	1501	CANCITAATITIACTICAGCCATCGTACCCTCTTCTGACTGATGGACC
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encoding novel human thymidylate kinase subfamily kinase.

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Kinase of the thymidylate kinase subfamily. The human kinase polypeptides and nucleic acid molecules are useful as models for the development of human therapeutic targets, aid in the identification of therapeutic broad molecules are useful as models for the development of human therapeutic proteins, or serve as targets for the development of human therapeutic proteins, or serve as targets for the development of human therapeutic contents. That modulate kinase activity in cells and tissues that express the kinase proteins are also useful in raising antibodies or eliciting another immune response, as reagents in assays designed to contain thatistively determine levels of the protein in biological fluids, as markers for tissues in which the corresponding protein is preferentially expressed, or in screening a compound for the ability to stimulate or influit interacts with the kinase protein and a molecule that normally interacts with the kinase protein and a molecule that corresponding or anglesase or a predisposition to a disease mediated by the diagnosing a disease or a predisposition to a disease mediated by the associated with the absence of inappropriate, or unwanted expression of the protein or nucleic acid molecule. Or for treating a discorder content or nucleic acid molecule. The antibodies are useful for tissue typing, in isolating or detecting kinase proteins, or in pharmacogenomic analysis. This sequence encodes the novel human
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ive 0; Mismatches
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Matches 2571, Conservative
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ABX93989 standard; cDNA; 2571 BP

(first entry)

10-JUN-2003

ABX93989

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The present invention provides human kinase polypeptides and the encoding polynucleotides. The invention is useful in the development of human therapeutic and diagnostic compositions, to identify therapeutic proteins and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues, to elicit an immune response and for diagnosing and treating disorders characterised by the absence of inappropriate and unwanted expression of the protein. The

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polypeptide is also useful in protein therapy. The present sequence is human kinase cDNA of the invention. The human kinase gene is located on chromosome 2.
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breast-specific proteins. The DNA and protein sequences of the invention are useful for the diagnosis, treatment and prevention of breast cancer. The present DNA sequence encodes a human breast-specific protein of the invention. Sequence 3060 BP; 731 A; 758 C; 757 G; 814 T; 0 U; 0 Other;	92.6%; Score 2380.6; DB 12; ty 99.4%; Pred. No. 0; ervative 0; Mismatches 9; I	15 GCGTCGCTGAGGCCCCTCGCCCGCCGGCTCCTGCGGGGCCACTGTCGGGGC 74	75 CGCTGCTCGGGGGGGGGGGGGTCTGCGCTGGCGCATGGCTCCGCGGTGCGCTTCGTCC 134	135 TGGAGCTTCCCGACTGCACCCTGGCTCACTTCGCCCTAGGCGCCGACGCCCGGGGAGG 194	195 CAGACGCCCCGGACCCCGCCTGGCGGCGCTGTTGGGGCCCCCGGAGCGCACTACTCGC 254	255 TGTGCGTGCCCGTGACCCCGGACGCCGGGCCCGGGGTCCGGGGCGGGGCGGCTGC 314 241 TGTGCGTGCCCGTGACCCCGGACGCCGGCTGCGGGCCCGGGCCGGCGCGCGC	315 ACCAGCGCTGCTGCACCAGCTGCGCCGCGCCCCTTCCAGCGGTGCCAGCTGCTCAGGC 374 301 ACCAGCGCCTGCTGCACCAGCTGCGCGGGCCCCTTCCAGCGGTGCCAGCTGCTGAGGC 360	375 TGCTCTGCTACTGCCCGGGCGGCCGGCGGCGGCGACAGCAAGCA	435 ACCCCTGGATGACCTGACACCGGCAAGGCTTGCTCGAGCTGCTGGCGCGCTGCCAGGCTGCCTGC	495 AGGCACCACGCCCGCACTTGGGCGAGTTCGAGGCCGACCCGCGGGCCAGCTGTGGCCAGCTGTGGCCAGCTGTGGGCAGCTTCGAGGCCGACCACCACCGCCGGCCACTTGGGCAGTTCGAGCCGACCGGCCGG	555 GCCTCTGGGAGGTGCAAGACGGCAGCTGCAGGTGGGCTGCGCACAGGTCGTGCCCG 614	615	675 ACCGGGAAGCCGCCGGGCCGTTTTGGAGGAGTGTACCTCTTTATTCCTGAAGCCCGGG 	735	795 TTGCCATCGAAGGACTGGATGCCACGGGTAAAACCACGGTGACCCAGTCAGT	B55 CACTTAAGGCTGTCCTCTTAAAGTCACCACCTCTTGCATTGGCCAGTGGAGGAAGATCT 914	915 TIGATGATGAACCAACTATCATTAGAAGAGCTTTTTACTCTTTGGGCAATTATATTGTGG 974
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                                                                                                                     ATATCATTTAGCCAATCCAGTAATTTATTTATTTAATCTATACATAATATGTTTCCTCA
                          TGAACTGGATGC
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/product= "kinase and phosphatase KPP-17"
                                                            TCTTTTTTTCTAAAGAATTGGCTCTGAATAGAATGCACAT
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2002US-0400509P.
2002US-0400783P.
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                                                                                                                                                                                                                                                                          New human kinases and phosphatases, useful for diagnosing, treating or preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
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                                                      Richarus, Knars Griffin JA, Knars Tran rnakar A, Chawla NK, Tran rnakar A, Forsythe IJ, I
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                                        , Kable AB, n.
PG, Lee SY, Grit.
PR, Swarnakar A, c..
Thornton MB, Fr
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                                                               A, Emerling BM, Kable Aus,
Tang YT, Lal PG, Lee SY,
S, Jin P, Hawkins PR, Swa:
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Best Local Similarity 98.2
Matches 2440; Conservative
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Ramkumar J;
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                                                                                    Hafalla ... Eaughn MR, Tan
Elliott VS, Ji
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Gietzen KJ,
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01-MAY-2002; 2002US-00136826.
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 antisense; WNT-7B; N-acetylglucosaminyltransferase; voltage-gated potassium channel; ion transport; Map3X8; thymidine kinase; cell proliferation; H-Ras; small interfering RNA; siRNA; embryogenesis; carcinogenesis; tumour progression; cell migration; matrix invasion; cell differentiation; stress response; cytostatic; antiinflammatory; cardiac arrhythmia; neurological disorder; epilepsy; interleukin 1b;
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/note=""Forms double stranded region with nucleotides 20-
1 of sequence in {seqid:33}"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'bound moiety= "CG94235-01-TK-AS5"
'note=""Forms double stranded region with nucleotides 20-
! of sequence in {seqid:37}"
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/note= "Forms double stranded region with nucleotides
1 of sequence in {seqid:34}"
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/note=""Forms double stranded region with nucleotides
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/note= "Forms double stranded region with nucleotides
1 of sequence in {segid:36}"
1297. .285
                                                                                                                                            Thymidine kinase DNA, a target for antisense inhibition.
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/*tag= b
/product= "Thymidine kinase protein"
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                                   2470 CTTGTGTGACTTTAGGGAGTAGCT 2493
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04-DEC-2001; 2
02-APR-2002; 2
02-APR-2002; 2
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The invention feature to inverse displacements the voltage gated potassium channel, ion transport, Map3KB or thymidine kinase. Specifically, the invention describes inhibiting cell proliferation by modulating the function of oncology targets: H-Ras, WNT-7B and acetylglucosaminyltransferase. Small interfering RNA (siRNA) along with the antisense compounds specifically hybridise to the target nucleic acid molecules to inhibit gene expression. The WNL proteins are secreted ligands involved in embryogenesis and carcinogenesis, such that these antisense obligos are useful for treating breast, gastric and colon cancers. N-acetylglucosaminyltransferases are associated with tumour progression, cell migration and matrix invasion, while Map3KB regulates cancers the disorders responses, such that antisense inhibitors are cytostatic and antifinflammatory, and can be useful in cell offferential and modulates electrical excitability in neurons and can be useful in the treatment of cardiac arrhythmias and neurological disorders such as epilepsy. Thymidine kinase is important in DNA synthesis, and antisense compounds can treat cell proliferation and modulate the expression of interleukin B to inhibit their expression. This polymucleotide sequence interleukin B to inhibit expression. This polymucleotide sequence
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Pred. No. 0;
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Best Local Similarity 98.9
Matches 2388; Conservative
                                                                                                                                                C, Zhong F
Smithson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New oligonucleotides,
inhibit expression of
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-697551/66.
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 The invention relates to new isolated NovX polypeptides, the genes encoding them or sequences having at least 95% identity to the amino acid or nucleotide sequences. The NovX polypeptide is useful as a therapeutic, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with a human disease, which includes a pathology associated with novX polypeptide. The NoVX polypeptide is particularly useful for treating, preventing or alleviating pathology associated with NoVX to polypeptide in a mammal, e.g. a human. The NoVx nucleic acid and polypeptide are especially useful for treating or preventing e.g. diabetes, obesity, cancers (e.g. lymphona, uterus cancer or prostate cancer), dyslipidemias, anorexia, asting disorders, Alzheimer's disease, parkinson's disorder, canceria, ca

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New NOVX polypeptides and polynucleotides, useful in gene therapy, particularly for treating or preventing a syndrome associated with a human disease e.g. diabetes, obesity, cancer, Alzheimer's disease,
                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
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18-OCT-2001;
28-NOV-2001;
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17-AUG-2001;
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2001US-0313416P. 2001US-0318463P. 2001US-0325683P. 2001US-0330292P.

2001US-0333873P. 2001US-0336909P. 2001US-0337552P.

2002US-00136826 2002US-0359245P

Rastelli L, Ellerman K;

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antilipemic; nootropic; neuroprofective; immunostimulant; antiparkinsonian; anti-HIV; antiasthmatic; antiinflammatory; hypotensive; antiarteriosclerotic; hemostatic osteopathic; gene therapy.; NOVX; diabetes; obesity; cancer; lymphoma; uterus cancer; prostate cancer; dyslipidemia; anorexia; wasting disorder; Alzheimer's disease; crock; cachexia; cardiomyopathy; AIDS; asthma; crohn's disease; multiple sclerosis; hypertension; atherosclerosis; hemophilia; graft-versus-host disease;
ds, gene, antidiabetic; cytostatic; immunomodulator; anorectic; antilipemic; nootropic; neuroprotective; immunostimulant;
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28. .1294
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0; Mismatches Score 2276; Pred. No. 0;

88.5%; 98.9%;

Query Match Best Local Similarity 98.9 Matches 2388; Conservative

DB 10; Length 2856;

Sequence 2856 BP; 700 A; 712 C; 692 G; 752 T; 0 U; 0 Other;

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ID NO 77; 748pp; English

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Claim 20;

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Kekuda R; Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL; Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR; Bllerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman LI, Gorman LI, Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R; Khramtsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR; Maclachlan T, Malyankar UM, Mcqueeney K, Mezick AJ, Miller CE; Millet I, Padigaru M, Patturajan M, Peyman AJ, Qian X, Rastelli L; Rieger DK, Stohe DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ; Wolenc AR, Zhong M, Zhong H;

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WPI; 2004-053467/05. P-PSDB; ADH42559

The invention relates to 566 new isolated human polypeptides and their encoding genes, sequences that are at least 954 identical to these or sequences comprising one or more conservative substitutions in these. The polypeptide, polymucleotide and antibodies against the polypeptides are useful in diagnosing, treating or preventing NoVX-associated disorders, e.g. cardiomyopathy, atheroselerosis, hypertension, cancer, obesity, diabetes, AIDS, multiple sclerosis, graft-versus-host disease.

Alzheimer's disease, parkinson's disease, asthma, or fertility disorders. The nucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The example of the nucleic acid sequence of the invention. nucleic acid molecules useful for preventing or New NOVX polypeptides and nucleic acid molecules useful for preventing of treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, in chromosome mapping, tissue typing or in Claim 20; SEQ ID NO 1111; 1503pp; English. pharmacogenomics.

Sequence 2856 BP; 700 A; 712 C; 692 G; 752 T; 0 U; 0 Other;

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GAAGGACTGGATGCCACGGGTAAAACCAAGGTGACCCAGTCAGTGGCAGATTCACTT 8	TAALIAILAITAGAAGAGCITTITAGTCTTTTGGGCAATTGTATGTGTGG TAAAGAATCTGCCAATCTCTGTGATTGTAGACAGGTACTGGCACA TAAAGAATCTGCCAAATCTCCTGTGATTGTAGACAGGCACA TGCCATAGCCACTGAGGTGAGTGGGGGGTCTCCAGCACCTGCCCCCAG	occordinations of the control of the	1220 GAAGCAGAACTTGAGGCCAACAGTGTGTTTCGTCAAAAGGTAGAAATGTCCTACCAGCGG	A CAGTATTAAGCCTAATCCAGAATAGTTTTAGTGAACCGTAGTTACTCTGGCCAGGTGCC	1460 TCCCAAATTTCTGTTCTACAAGCATGTTGTGGCAGAAAACTGGAGACCAGGCATCTTA 1519	CTCATCATGTTCCAGTGAGGCCAGCGATTGCTTTCTTCCTGGCATAGTAACATTTTC 163	CCAGATCAGCAGGGAGACCC CCTGACATGCCCACATTGGC CCTGACATGCCCACATTGGC CCTGACATGCCCACATTGGC CCTGACATCGCCCAAA SCATCTCCCTCAGTCCCAAA SCATCTCCCTCAGTCCCAAA

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The invention relates to an oligonucleotide (antisense) 20-50 or 10-50 nucleotides in length that is targeted to regions of the cDNAs appearing as ABM10596-ABM10601 (human WAT-7B, N-acetyglucosaminyltransferase, oltered Kinase kinase kinase 8) or thymidine kinase. Also included are protein kinase kinase kinase 8) or thymidine kinase. Also included are methods of inhibiting the expression of WAT-7B, N-acetyglucosaminyltransferase, voltage-gated K channel, ion transport, acetyglucosaminyltransferase, voltage-gated K channel, ion transport, MapXR8 or thymidine kinase in a cell, comprising contacting the cell with the oligonucleotide cited above, a method of inhibiting cell comprising contacting a cell with the oligonucleotide contacting a cell with the oligonucleotide cited above). Also disclosed are antisense oligonucleotide cited above). Also disclosed are antisense oligonucleotide for H-ras and interleukin-8. The antisense oligonucleotide is useful in modulating the expression of WMT-7B, N-acetyglalocaminal parts and interleukin-8. The antisense
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acetylglucosaminyltransferase, voltage-gated K channel, ion transport channel, map3K8 or thymidine kinase to treat diseases associated with their expression, such as cell proliferative disorders, infection or inflammation. In addition, the composition is used for disponstics, prophylaxis, or as research reagents or kits. The present sequence is cDNA from one of the ganes listed above, a target for the antisense oligonucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tisense oligonucleotide for modulating expression of WNT-7B, N-3lucoaminyltzansferase, voltage-gated K channel, ion transport, or thymidine kinase, or for treating cancer, infection or
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Millet I;
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BP.

Human cDNA #720 differentially expressed in activated vascular tissue.

Human, gene, ss; vascular tissue, cytostatic, atherosclerosis, cardiant, hypotensive, antidiabetic, gynaecological, vasotropic; cerebroprotective, gene therapy, vascular disease, cancer, coronary, artery disease, hyportension, diabetes, pre-eclampsia, restenosis, ischaemia-reperfusion injury, stroke.

Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several cDNAs that are differentially expressed in activated

This invention relates to a combination comprising several cDNAs that are differentially expressed in activated vascular tissue. The invention also discloses a high throughput method for detecting differentially expressed cDNAs in a sample. The CDNAs of the invention may have antiatteriosclerotic; cytostatic; cardiant; hypotensive; antidiabetic; gynaecological; vasotropic and cerebroprotective activities and may be used in gene therapy. The CDNAs of the invention may be used in a high-throughput methods for detecting differential expression of one or more CDNAs in a sample, or screening several molecules or compounds to identify a molecule or compound that specifically binds a cDNA of the invention. A protein encoded by the CDNA may be used to screen several molecules or compounds to identify a ligand that specifically binds to the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or

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          diagnoshing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary artery disease, hypertension, diabetes, pre-eclampsia, ischaemia-reperfusion injury, restenosis, or stroke. The cDNAs can also be used for large-scale genetic or gene expression analysis of several new nucleic acid molecules. Antibodies to the proteins encoded by the cDNAs are useful for diagnosing pre-pathologic disorders, and chronic or acute diseases associated with abnormalities in the expression, amount or distribution of the protein. The present sequence represents a cDNA of the invention that is differentially expressed in activated vascular tissue. Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly from USPTO at http.seqdata.uspto.gov/sequence.html?DocID=20020137081
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31-MAY-2001;
12-JUL-2001;
31-JUL-2001;
14-AUG-2001;
17-AUG-2001;
         25-MAY-2001;
29-MAY-2001;
29-MAY-2001;
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                                                                            CAGTAATTTATTTAATCTATACATAATATGTTTCCTCAGCATAGGAGCTATGATT
                                                                CAAACTTAATTTGTCTTGTTAAATAAGTTCAAGTGGATCTTGGAGTGGGATTTCTTGGTA
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                             CAGTAATTTATTTATATTAATCTATACATAATATGTTTCCTCAGCATAGGAGCTATGATT
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Albright hereditary osteodystrophy.
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2001US-0289087P.
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11-MAY-2001;
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15-MAY-2001;
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The invention relates to new isolated NOVX polypeptides, the genes encoding them or sequences having at least 95% identity to the amino acid or nucleotide sequences. The NOVX polypeptide is useful as a therapeutic, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide. The NOVX polypeptide is particularly useful for treating, preventing or alleviating pathology associated with NOVX polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and treating, preventing or alleviating pathology associated with NOVX polypeptide are especially useful for treating or preventing e.g. diabetes, obesity, cancers (e.g. lymphona, uterus cancer or prostate cancer), dyslipidemias, anorexia, wasting disorders, Alzheimer's disease, arkinson's disorder, canceria, cardiomyopathy, AlDS, asthma, Crohn's disease multiple sclerosis, hypertension, atherosclerosis, hemophilia, graft-versus-host disease or Albright hereditary osteodystrophy. The DNA conditions. These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications. This sequence represents one of the NOVX genes of the
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M, Anderson DW, Mezes PS, Peyman JA, Macdougall JR;
Rastelli L, Shenoy SG, Gerlach VL, Shimkets RA, Zhong
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28-NOV-2001; 2001US-0333873P.
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2001US-0294827P.
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(CURA-) CURAGEN CORP.

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WPI; 2004-053467/05. P-PSDB; ADH42565.

ö New NOVX polypeptides and nucleic acid molecules useful for preventing treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, in chromosome mapping, tissue typing or in

1029 1149 1269 encoding genes, sequences that are at least significant to these or sequences comprising one or more conservative substitutions in these. The polypeptide, polynelectide and antibodies against the polypeptides are useful in diagnosing, treating or preventing NOVX-associated disorders, diabetes. AIDS, multiple sclerosis, hypertension, cancer, obesity, Alzhenmer's disease, asthma, or fertility disorders. The mucleic acids are further used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The polypeptides are also useful as vaccines. This sequence represents an example of the nucleic acid sequence of the invention. 7; 1089 GCTGCTCACTGTGAGTCCTGAGGAGAGATTGCAGAGGCTGCAGGGCCGGGGCATGGAGAA 1209 1389 GCCAGGTGCCACGTCTAACTAGATTAGATGTTGTGAAACATCTACATCCACCATTGT 1449 479 729 599 119 789 606 696 359 419 539 179 849 239 629 719 779 invention relates to 566 new isolated human polypeptides and their 300 GATCTTTGATGATGAACCAACTATCATTAGAAGAGCTTTTTACTCTTTGGGGGAATTATAT CCTGGCTCACTTCGCCCTAGGCGCCCGTTTTGGAGGAGTGTACCTCCTTTATTCCTGAAGC CCGGGCAGTGCTTGACCTGGTCGACCAGTGCCCAAAACAGAAAGGAAAGGAAAGTTCCA 180 defirir de la controla del la controla del la controla del la controla del la controla de la controla del la controla del la controla del la controla del la controla del la controla del la controla del la controla del la controla del la controla del la controla del la con AGATTCACTTAAGGCTGTCCTCTTAAAGTCACCACCCTCTTGCATTGGCCAGTGGAGGAA 910 GATCTTTGATGAACCAACTATCATTAGAAGAGCTTTTTACTCTTTGGGCAATTATAT 970 TGTGGCCTCCGAAATAGCTAAAGAATCTGCCAAATCTCCTGTGATTGTAGACAGGTACTG 360 TGTGGCCTCCGAAATAGCTAAAGAATCTGCCAAATCTCCTGTGATTGTAGAACAGCTACTG 1030 GCACAGCACGCCACCTATGCCATAGCCACTGAGTGAGTGGGGGGTCTCCAGCACCTGCC 420 GCACAGGACGGCCACCTATGCCATAGCCACTGAGGTGAGTGGGGGTCTCCAGCACCTGCC CCCAGCCCATCACCTGTGTACCAGTGGCCAGAGGACCTGCTCAAACCTGACCTTATCCT GACCAGGGAAGAAGCAGAACTTGAGGCCAACAGTGTGTTTCGTCAAAAGGTAGAAATGTC CCCGGACCGGGAAGCCGCCCGGCCGTTTTGGAGGAGTGTACCTCCTTTATTCCTGAAGC 540 GCTGCTCACTGTGAGTCCTGAGGAGAGGTTGCAGAGGCTGCAGGGCCGGGCCATGGAGAA AGATTCACTTAAAGGCTGTCCTCTTAAAGTCACCACCCTCTTGCATTGGCCAGTGGAGGAA GACCAGGGAAGAAGCAGAACTTGAGGCCAACAGTGTGTTTCGTCAAAAGGTAGAAATGTC CTACCAGCGGATGGAGAATCCTGGCTGCCATGTGGTTGATGCCAGCCCCTCCAGAGAAAA GGTCCTGCAGACAGTATTAAGCCTAATCCAGAATAGTTTTAGTGAACCGTAGTTACTCTG 480 céchécécarchécérérérandeséchésésésésésérendenésérendesérentarien CTACCAGCGGATGGAGAATCCTGGCTGCCATGTGGTTGATGCCAGCCCTCCAGAGAAA GGTCCTGCAGACGGTATTAAGCCTAATCCAGAATAGTTTTAGTGAACCGTAGTTACTCTG Gaps DB 12; Length 2331; 7; Sequence 2331 BP; 646 A; 502 C; 497 G; 686 T; 0 U; 0 Other; Indels 22; Query Match 66.3%; Score 1704.8; Best Local Similarity 98.4%; Pred. No. 0; Matches 1795; Conservative 0; Mismatches Claim 20; SEQ ID NO 1117; 1503pp; English Query Match Best Local Similarity pharmacogenomics 0.29 09 850 240 730 790 1090 1150 1210 1270 1330 009 099 720 1390 qq g à d ò 8 à g à Db q ò à g ò g 8 g δ 임 δ g

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This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular corganisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information received from other cells and the immediate environment. The information of the transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, cautopeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such are receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention corrections of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be cuseful for the mannifacture of a medicament for diagnosing or treating at tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New PRO polypeptides, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis
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                                                                                                                                                                              human, PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; cytotoxic factor; differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour;
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Williams PM,
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                                                                          ADF76970;
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RESULT 13
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Gaps DB 10; Length 2566; 13; Indels Score 1694.2; I Pred. No. 0; 0; Mismatches Query Match
Best Local Similarity 98.9%;
Matches 1779; Conservative

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MILLENNIUM PREDICTIVE MEDICINE INC.
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WPI; 2001-662795/76

with cancerous state of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer Novel isolated nucleic acid molecule associated prostate cells and correlating with presence of

Claim 1; Page 5416-5417; 11750pp; English

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the factory of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker

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6 Other; Sequence 2199 BP; 597 A; 488 C; 516 G; 592 T; 0 U;

1234 1294 1054 1114 1174 TGCCATGTGGGTTGATGCCAGGCCCTCCAGAGAAAAGGTCCTGCAGACAGTATTAAGCCTA 1354 486 909 786 13; 994 426 814 306 874 366 934 754 AGGTTGCAGAGGCTGCAGGGCCGGGGCATGGAGAAGACCAGGGAAGAAGCAGAACTTGAG cagrecccaaaacagarccagaaaggaaagrrccaggrrgrrgccarcgaaggacrggar eccaceegraaaaccaceereaccacroacroacreecagarroacrraagecrercrra AAGTCACCACCTCTTGCCATTGGCCAGTGGAGGAAGATCTTTGATGATGAACCAACTATC ATTAGAAGAGCTTTTTACTCTTTGGGCAATTATATTGTGGCCTCCGAAATAGCTAAAGAA TCTGCCAAATCTCCTGTGATTGTAGACAGGTACTGGCACAGCACGGCCACATATGCCATA TCTGCCAAATCTCCTGTGATTGTAGACAGGTACTGGCACAGCACGGCCACCTATGCCATA GCCACTGAGGTGAGGGGGTCTCCAGCACCTGCCCCCAGCCCATCACCCTGTGTACCAG TGGCCAGAGGACCTGCTCAAACCTGACCTTATCCTGCTGCTCACTGTGAGTCCTGAGGAG TGGCCAGAGGACCTGCTCAAACCTGACCTTATCCTGCTGCTCACTGTGAGTCCTGAGGAG AGGTTGCAGAGGCTGCAGGGCCGGGGCATGGAGAAGAAGAAGAAGAAGAAGTTGAG GCCAACAGTGTGTTTCGTCAAAAGGTAGAAATGTCCTACCAGCGGATGGAGAATCCTGGC GCCAACAGTGTTTCGTCAAAAGGTAGAAATGTCCTACCAGCGGATGGAGAATCCTGGC gecachdaggrdagrdagggrcrccagcaccrdccccdagcccarcaccrgraracag GITITGGAGGAGTGTACCTCCTTATTCCTGAAGCCCGGGCAGTGCTTGACCTGGTCGAC ecrigidecacadidiaccicciriarifichdaadcccdddcagictigaccidgicdac CAGTGCCCAAAACAGATCCAGAAAGGAAAGTTCCAGGTTGTTGCCATCGAAGGACTGGAT GCCACGGGTAAAACCACGCTGACCCAGTCAGTGGCAGATTCACTTAAAGGCTGTCCTCTTA 367 AAGTCACCACCTCTTGCATTGGCCAGTGGAGGAAGATCTTTGATGATGAACCAACTATC Gaps 18; DB 5; Length 2199; Indels Score 1579.6; DB 5; Pred. No. 2.5e-306; 0; Mismatches 34; 61.4%; 97.1%; Conservative Query Match Best Local Similarity Matches 1748; Conserv 547 487 1115 1175 1235 1055 667 247 875 935 427 995 607 695 187 755 815 307

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TTAICTIGCACTIGAAIGICICCIGAITACATATGAAAICGC-IIGACAIAICITIGGAC 1909
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                                                                                                                                                                                                                                                                          cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                              Sequence 2199 BP; 597 A; 488 C; 516 G; 592 T; 0 U; 6 Other;
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                                               Gaps
                                             18;
       DB 5; Length 2199;
                                           34; Indels
     Score 1579.6; DB 5;
Pred. No. 2.5e-306;
0; Mismatches 34;
Query Match 61.4%;
Best Local Similarity 97.1%;
Matches 1748; Conservative
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TGCAGAGGCTGTCTATGTGTCCTGGCTGCCCAAGGGACACTCCTGCAGAGCCAT 	TCTTGTGT	GTAAGGAACACTTACAAAGAAGCATTGATCTTGTGTCTGAGGCT	AGGCTTCTGATGTCATAAAAGACATTCAAGCCAAGAT	AGGCTTCTGA-GTCATATATAAAGACATTCAAGCCAAGATGCTCCAACTGCAAATATACC	AACCTICTCTGAALTATATTTTGCTTATTATATTTCTTTTCTTTTTTTTTT	AA-CTTCTTTTTTTTTATA-TTTGCTTATTTATATTTCTTTTTTTTTT	GCTCTGAATAGAATGCACATTTTCCATCTGAACTGGATGCA	GCTCTGAATAGAATGCACATTTCCAT-TGAACTGGATGCATTT	TAATITATITATATAATCATACATAATATATGCTCA	TAATTTATTTATTTAATTTAATCTATACATACTATACT	TAATTAAAAGTGGAGTCAAAACGCTAAATGCAATGTTTGT	TAATTAAAAGTGGAGTCAAAA-GCTAAATGCAATGTC	ACTIAATTIGICTIGITAAATAAGTICAAGIGGAICTIGGAGIGGGATITCIT	ATTAATTGTCTTGTTAATAAGTACAGGGATCTTGC	TTATCTTGCACTTGAATGTCTCATGATTACATATGAAATCG	TTATCTTGCACTTGAATGTCTCCTGATTACATATGAAATCG	AGAAAAAAGCTGAGTGAGGGGGAAATTATAGAGCTTGTGTGA	AGAAAAAAGTAGTGAGTGAGGGGGAAATTATAGAGGCTGTGTGACTTTAGGGGAGTAGGT
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Search completed: October 22, 2004, 15:07:42 Job time: 1235 secs

Title: Perfect score:

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1 (bases 1 to 2571)

Wei,M.-H., Ketchum,K.A., Beasley,E.M. and DiFrancesco,V.
Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof
Patent: US 6489153-A 1 03-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCACTGTCGGGGCCGCTGCTCGGGCGCGGGGGTCTGCGCTGGGGCCCATGGCTCCGCC
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Sequence 1 from patent US 6489153.
AR258675 GI:27309061
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    mol_type="genomic DNA"

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KEYWORDS
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Listing first 45 summaries
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CAGGTCGTGCCGGTCCCGGTGCACCCGGTGGTGCCAGACTTGCCCAGTTC [CCAAAACGGTCC7 5GTAAAACCACGGT 3GTAAAACCACGGT CCACCTCTTGCAT	3AAGAGCTTTTTACTCTTTGGG 3AAGAGCTTTTTACTCTTTGGG CCAAATCTCCTGTGATTGTAGA		1141 CCTTATCCTGCTCACTGTGAGTCCTGAGGAGGTTGCAGAGGAGCTGGCTCAAACCTGA 1140 1141 CCTTATCCTGCTGCTGAGGAGTCCTCAGGAGGAGGTTGCAGAGGCTGCAGGGCCGGGG 1200 1141 CCTTATCCTGCTGCTGTGAGTCCTGAGGAGGTTGCAGAGGCTGCAGGGCCGGGG 1200	1201 CATGGAGAAGAAGAAGAAGTTGAGGCCAACAGTGTGTTTGTCAAAAGGT	61 AGAAATGICCTACCAGGGGATGGAGAATCCTGGCTGCCATGTGGTTGATGCCAGCCCCT 21 CAGACAAAAGGTCCTGCAGACAGTATTAAGCCTAATCCAGAATAGTTTTAGTGAACCGT 21 CAGAGAAAAGGTCCTGCAGAAGTATTAAGCCTAATCCAGAATAGTTTTAGTGAACCGT 21 CAGAGAAAAGGTCCTGCAGAAGTATTAAGCCTAATCCAGAATAGTTTTAGTGAACCGT	1381 GTTACTCTGGCCAGGTGCCACGTCTAACTAGATTAGATGTTGTTTGAACATCTACATCC 1440	41 ACCATTGTTATGCAGTGT 41 CTGGAGACCAGGCATCTA 01 CTGGAGACCAGGCATCTTA 01 CTGGAGACCAGGCATCTTA	1561 GGTCATCACAAAGGTCCCTCATCATGTCCAGTGACAGCCAACCGATTGCTTTCTTCC 1620
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AUTHORS Schlegel,R., Endege,W.O. and Monahan,J.E. TITLE Genes differentially expressed in human prostate cancer and their use JOURNAL Patent: WO 0160860-A 20954 23-AUG-2001; Millennium Predictive Medicine, Inc. (US) FEATURES 1. 2199 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match 61.4%; Score 1579.6; DB 6; Length 2199; Best Local Similarity 97.1%; Pred. No. 9.1e-247; Matches 1748; Conservative 0; Mismatches 34; Indels 18; Gaps 13;	9y 695 GITIIGGAGGAGIGIACCICCIIIAIICCIGAAGCCGGGCAGIGCIIGACCIGGICGAC 754			ο 4		QY 995 TCTGCCAAAICTCCTGTGATTGTAGACAGGTACTGGCACGGCCGCCTATGCCATA 1054		OY 1115 TGGCCAGAGGACCTGCAAACCTGACTGCTGCTGCTGAGGGGGGGG		OY 1235 GCCAACAGTGTGTTTCGTCAAAAGGTAGAAATGTCCTACCAGCGGATGGAGAATCCTGGC 1294	OY 1295 TGCCATGTGGTTGATGCCAGCCCCTCCAGAGAAAAGGTCCTGCAGACAGTATTAAGCCTA 1354	Qy 1355 ATCCAGAATAGTTTTAGTGAACCGTAGTTACTCTGGCCAGGTGCCACGTCTAACTAGATT 1414	1415	QY 1475 CTACAAGCATGTTGTGGCAGAAAACTGGAGACCAGGCATCTTAATTTTACTTCAGCCA 1534 Db 967 CTACAAGCATGTTGTGGCAGAAAACTGGAGAACCAGGCATCTTAATTTTACTTCAGCCA 1026
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Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

EUKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS Schlegel,R., Endege,W.O. and Monahan,J.E. Genes differentially expressed in human prostate cancer and their use JOURNAL Patent: WO 0160860-A 22065 23-AUG-2001; Millennium Predictive Medicine, Inc. (US) FEATURES 1. 2199 //organism="Homo sapiens" //mol_type="unassigned DNA" ORIGIN	Query Match 61.4%; Score 1579.6; DB 6; Length 2199; Best Local Similarity 97.1%; Pred. No. 9.1e-247; Matches 1748; Conservative 0; Mismatches 34; Indels 18; Gaps 13;	Oy 695 GTITIGGAGGAGTGTACCTCCTITATICCTGAAGCCCGGGCAGTGCTTGACCTGGTCGAC 754	OY 755 CAGTGCCCAAAACAGATCCAGAAAGGAAAGTTCCAGGTTGTTGCCATCGAAGGACTGGAT 814 Db 247 CAGTGCCCAAAACAGATCCAGAAAGTTCCAGGTTGTTGCCATCGAAGGAT 306	OY 815 GCCACGGGTAAAACCACGGTGACCCAGTCAGTGGCAGATTCACTTAAGGCTGTCCTCTTA 874	OY 875 AAGTCACCACCTCTTGCATTGGCCAGTGGAGGAAGATCTTTGATGAACCAACTATC 934	Qy 935 ATTAGAAGACTTTTTACTCTTTGGGCAATTATATTGTGGCCTCCGAAATAGCTAAAGAA 994	QY 995 TCTGCCAAATCTCCTGTGATTGTAGACAGGTACTGGCACAGGCCACCTATGCCATA 1054	QY 1055 GCCACTGAGGTGAGGGGTCTCCAGCACCTGCCCCCAGCCCATCACCTGTGTACCAG 1114	QY 1115 TGGCCAGAGGACCTGCTCAAACCTGACCTTATCCTGCTGACTTGTGAGTCCTGAGGAG 1174 Db 607 TGGCCAGAGGACCTGCTCAAACCTGACCTTATCCTGCTGCTGTGAGTCCTGAGGAG 666	Qy 1175 AGGTIGCAGAGCTGCAGGGCCTGGGGCATGGAGAAGAAGAAGAAGAAGAACATGAG 1234 Db 667 AGGTIGCAGAGCTGCAGGGCCTGGAGCATGAAGAAGAAGAAGAAGAAGAAGAAGAACTTGAG 7.26	OY 1235 GCCAACAGTGTGTGTCAAAAGGTAGAAATGTCCTACCAGCGGATGGAGAATCCTGGC 1294	Oy 1295 IGCCAIGTGAIGCCAGCCCCTCCAGAGAAAAGGTCCTGCAGACAGIAITAAGCCIA 1354	0y 1355 AICCAGAATAGTITIAGTGAACCGTAGTTACTCTGGCCAGGTGCCACGTCTAACTTAGTT 1414	QY 1415 AGAIGTIGTITGAAACAICTACAICCACCAITIGITAIGCAGIGTICCCAAAITICIGII 1474	OY 1475 CTACAAGCATGTTGTGGCAGAAAACTGGAGACCAGGCATCTTAATTTTACTTCAGCCA 1534
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KEYWORDS SOURCE Homo sapiens (human) SOURCE Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS Schlegel,R., Endege,W.O. and Monahan,J.E. TITLE Genes differentially expressed in human prostate cancer and their JOURNAL Patent: WO 0160860-A 26800 23-AUG-2001; Millennium Predictive Medicine, Inc. (US) FEATURES Location/Qualifiers Source //mol_type="Homo sapiens" //mol_type="unassigned DNA" //db_xref="taxon:9606"	Query Ma Best Loc Matches	81 30 87	Db 307 GCCACGCGTAAAACCACGGTGCCAGTTGTTTTAATTTAA	105 546	OY 1055 GCCACTGAGGTGAGGGGTCTCCAGCACCTGCCCCAGCCCATCACCTGTGTACCAG 1114	QY 1115 TGGCCAGAGGACCTGCAGACCTGACTGCTGCTGCTGACTCCTGAGGAG 1174 Db 607 TGGCCAGAGGACCTGACCTGACCTTATCCTGCTGCTGTGAGTCCTGAGGAG 666	QY 1175 AGGTTGCAGAGGCTGCAGGGCATGGAGAAGACGAGAACTTGAG 1234 Db 667 AGGTTGCAGAGGCTGCAGGGCATGGAGAAGAACACAGGAAAGAACCAGAACTTGAG 726	QY 1235 GCCAACAGTGTGTTTCGTCAAAAGGTACAAATGTCCTACCAGCGGATGGAGAATCCTGGC 1294	Oy 1295 TGCCATGTGGTTGATGCCAGCCCCTCCAGAGAAAGGTCCTGCAGACAGTATTAAGCCT 1354	QY 1355 AICCAGAATAGTTTTAGTGAACCGTAGTTACTCTGGCCAGGTGCCACGTCTAACTAGATT 1414 Db 847 AICCAGAATAGTTTTAGTGAACCGTAGTTACTCTGGCCAGGTGCCACGTCTAACTAA
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/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Ouery Match 52.0%; Score 1336.6; DB 6; Length 1343; Best Local Similarity 99.7%; Pred. No. 2.8e-207; Matches 1339; Conservative 0; Mismatches 4; Indels 0; Gaps	32. A L L	Qy 92 GGGGTCTGGGCTGGGCCATGGCTCGCGTGCGCTTCGTCCTGGAGCTTCCCGACTGC 151	QY 152 ACCTGGCTCACTTCGCCCTAGGCGCCGCGCGCGCGCGCGC	Qy 212 CGCCTGGCGGCGCTGTTGGGGCCCCCGGAGCTACTCGCTGTGCGTGC	QY 272 CCGGACGCGGCTGCGGGTCCGGGTCCGGGCTGCACCACGCCTGCTGCAC 331 Db 241 CCGGACGCCGGCTGCGGGTCCGGGCTCCGGGCTGCACCAGCGCTGCTGCAC 300	Oy 332 CAGCTGCGCCGCCCTTCCAGCGCTGCTGCTCAGGCTGCTCTGCTACTGCTACTGCCGG 391	QY 392 GGCGGCCAGGCCGCGCACAGCACAGCAAGCAAGCACTCCTGCCCCCCTGGATGACCCT 451	QY 452 GACACCGGCAAGGCTTGCTGGGGGGGCTTGCCAGGAGGCACCACGCCCGCAC 511	Qy 512 TTGGGCGAGTTCGAGGCCGACCCGCGGCCAGCTGTGGCAGCGCTCTGGGAGGTCCAA 571 Db 481 TTGGGCGAGTTCGAGGCCGACCCGCGGCCGAGCTGTGGCACCTCTGGGAGGTGCAA 540	QY 572 GACGGCAGGCGGCTGCAGGTGCGCACAGGTCGTGCCGTGCCGGAGCCCCGGTG 631	QY 632 CACCGGTGGTGCCAGACTTGCCCAGTTCCGTGGTCTTCCCGGACCGGGAAGCCGCCGG 691	QY 692 GCGTTTTGGAGGAGTGTACCTCCTTTATTCCTGAAGCCCGGGCAGTGCTTGACCTGGTC 751 DD 661 GCGTTTTGGAGGAGTGTACCTCCTTTATTCCTGAAGCCCGGGCAGTGCTTGACCTGGTC 720	Oy 752 GACCACTGCCCAAAACAGATCCAGAAAGTTCCAGGTTGTTGCCATCGAAGGACTG 811	Oy 812 GATGCCACGGGTAAAACCACGGGACCCAGTCAGTCACTTAAGGCTGTCCTC 871	872 TIAAAGTCACCACCTCTTGCATTGGCCAGTGGAGGAAGATCTTTGATGATGAACCAACT	Db 841 TTAAAGTCACCACCTCTTGCATTGGCCAGTGGAGGAAGATCTTTGATGAACCAACT 900 932 ATCATTAGAAGAGCTTTTTACTCTTTGGCAATTATATTGTGGCCTCCGAAATAGCTAAA 991	Db 901 ATCATTAGAAGACTTTTTACTCTTTGGGCAATTATATTGTGGCCTCCGAAATAAAA 960
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgo.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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Submitted (05-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 27 Row: n Column: 24.
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                                                                                        ATAGCCACTGAGGTGAGTGGGGGTCTCCAGCACCTGCCCCCAGCCCATCACCCTGTGTAC
             GAATCTGCCAAATCTCCTGTGATTGTAGACAGGTACTGGCACAGCACGGCCACCTATGCC
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1720)
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Homo sapiens, clone IMAGE:4428577, mRNA, partial cds.
BC016969
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/clone lib="NIH MGC 91"
/lab host="DH10B"
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NIH-MGC Project URL: http://mgc.nci.nih.gov
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4428577"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Homo sapiens
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Submitted (19-AUG-2001) Department of Genetics, Washington
Submitted (19-AUG-2001) Department of Genetics, Washington
Stiff of the Submitted of Submitted (19-AUG-2001) Department of Genetics, Missouri 63108, USA
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Submitted (07-NOV-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Feb 18, 2001 this sequence version replaced gi:11181849.
                                                                                                  1016 TGTTTCCTCAGCATAGGAGCTATGATTCATTAAATAGTGGAGTCAAAACGCTAAATG 1075
                                                                                                                                                                                                                                                                         1076 CAATGTTTGTTGTGTATTTTCATTACACAAACTTAATTTGTCTTTAAATAAGTAC-AG 1134
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                        898 ATATTTCTTTTTTTTTTTTTTTAAAGTA-TGGCTCTGAAATAGAATGCACATTTTCCAT-TG 955
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Catarrhini, Hominidae, Homo.
2105 ATAITTCTTTTCTTTTTTTTTTTAAAGAATTGGCTCTGAATAGAATGCACATTTTCCATCTG
                                                                                                                                                                                                                                    CAATGITIGITIGITATITITCATTACACAAACTITAATITIGICITGITAAAIAAGITCAAG
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Homo sapiens BAC clone RP11-439M11 from 2, complete sequence.
AC017076
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Tomlinson, C., Abbott, A. and Barrett, M.
The sequence of Homo sapiens BAC clone RP11-439M11
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Mammalia; Euthoria; Primates;
1 (bases 1 to 11808)
Sulston,J.E. and Waterston,R.
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Waterston, R.H.
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Waterston, R.H.
Direct Submission
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MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MC. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The clone sequenced to the left is RP11-445N10; the clone sequenced to the right is CTD-2016F17, 200 bp overlap. Actual start of this clone is at base position 1 of RP11-439M11; actual end is at base position 75906 of CTD-2016F17.

Location/Qualifiers

1. .118808
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                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to respect all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The RECI-II human BAC library was made from the blood of one male donor, as described by Oseogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catannese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                        entire insert of this
                                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this colone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                         Center: Washington University Genome Sequencing Center
                                          Center code: WUGSC
Web site: https://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                           Center project name: H_NH0439M11
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NEIGHBORING SEQUENCE INFORMATION:
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|mol_type="genomic DNA"
|db_xref="taxon:9606"
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8876. .8998
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clone_lib="RPCI-11"
[749. _1786
Genome Center
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/rpt_family="MIR"
3677. _4056
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5869. .600^
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9930_ .10164
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9668. .9892
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8218. .8358
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9289. .9482
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9168. .9250
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6979. .7055
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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41.4%; Score 1065.2; DB 6;
Best Local Similarity 89.8%; Pred. No. 3.5e-163;
Matches 1212; Conservative 0; Mismatches 3;
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PE Corporation (NY) (US)
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                                                                                            and Difrancesco, V.
                                                                                                                                                                                                                                                                      Length
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                                                                                            Beasley, E.M.
                      Unknown.
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 20966)
Wei,M.-H., Kerchum,K.A., Beasley,E.M.
Patent: US 6664087-A 316-DEC-2003;
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1. 20966
/organism="unknown"
/mol_type="genomic DNA"
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Matches 1228;
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Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S.,
Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai, Hio, Y., Satio, K., Nishikawa, T.,
Kimura, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Wagatsuma, M., Takahashi-Fuji, A., Oshima, A., Sugiyama, A.,
Rawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K.
NEDO human cDNA sequencing project
Unpublished
Unpublished
I cogai, T. and Yamamoto, J.
Direct Submission
Submitted (15-UUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
                                                                                                                                                                                 AK127983 1609 bp mRNA linear PRI 19-FEB-2004 Homo sapiens cDNA FLJ46098 fis, clone TBSTI2021654, weakly similar to Mus musculus thymidylate kinase family LPS-inducible member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NBDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and
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FALGADAPGDADAPDPRLAALLGPPERSYSLCVPVTPDAGCGARVRAARLHQRLLHQL
RRGPFQRCQLLRLLCYCPGGQAGGAQGGFLLRDPLDDPDTRQALLELLGACQEAPRPH
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ARAVLEECTSFIPEARAVLDLVDQCPKQIQKGKFQVVAIEGLDATGKTTVTQSVADSL
KAVPQPITLCTSGQRTCSNLTLSCCSL"
                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata, Craniata, Vertebrata, Buteleostomi, Primates, Catarrhini, Hominidae, Homo.
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/ organism="Homo sapiens"
/ organism="Homo sapiens"
/ db_xref="taxon:9606"
/ clone="TEST12021654"
/ tissue_type="testis"
/ clone_lib="TEST12"
/ note="floning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                    oligo capping; fis (full insert sequence)
Homo sapiens (human)
Homo sapiens
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Pred. No. 1.5e-134;
0; Mismatches 3;
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                           CIAATCCAGAATAGTTTTAGTGAACCGTAG 1215
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/db_xref="G1:34535132"
CTAATCCAGAATAGTTTTAGTGAACCGTAG
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llarity 83.4%;
Conservative (
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Mammalia; Eutheria;
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Best Local Similarity
Matches 1121; Conserv
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TITLE
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E. Consortium (LLNL)

at the Stanford Human Genome

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and Marra, M.A. CATGTGGTTGATGCCAGCCCCTC 1320 . linear ROD 25-JUN-2004 LPS-inducible member, mRNA complete cds. 1141 CCTTATCCTGCTGCTCACTGTGAGTCCTGAGGAGGGGTTGCAGAGGCTGCAGGGCCGGGG 1200 Vertebrata; Euteleostomi; thi; Muridae; Murinae; Mus. tutes of Health, Mammalian Office, National Cancer , Bethesda, MD 20892-2590, 16899-16903 (2002) vog.r ઠે

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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 15805017.
Location/Qualifiers
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                                   GCCCGTCCCGGAGCCCCCCCCGCTGCACCCGGTGCCAGACTTGCCCAGTTCCGTGGTCTT
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